GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 5, 2005, 07:39:13 ; Search time 5843 Seconds
(without alignments)
11294.883 Million cell updates/sec

Title: US-09-823-119B-3
Perfect score: 1362
Sequence: 1 atggcgctggtgcgcgcact.....atataaagcacaattactag 1362

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1362	100.0	1362	6	AX301999	AX301999 Sequence
2	1360.4	99.9	1759	9	BC018999	BC018999 Homo sapi
3	1360.4	99.9	1760	9	AK000184	AK000184 Homo sapi
4	1360.4	99.9	1764	6	AR113044	AR113044 Sequence
5	1360.4	99.9	1764	6	AR280051	AR280051 Sequence
6	1349.4	99.1	1746	6	AX281695	AX281695 Sequence
7	1341.4	98.5	2505	6	AX780232	AX780232 Sequence
8	1035.4	76.0	2049	6	CQ414095	CQ414095 Sequence
9	944.6	69.4	1758	6	AX305693	AX305693 Sequence
10	944.6	69.4	1758	10	MMASML3A	Y08135 M.musculus
11	936.4	68.8	1706	10	BC082029	BC082029 Rattus no
12	816.4	59.9	1095	6	AX302000	AX302000 Sequence
13	717.4	52.7	893	6	CQ717782	CQ717782 Sequence
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15	689	50.6	2842	5	AJ719446	AJ719446 Gallus ga
16	655.8	48.1	733	6	BD221211	BD221211 Human gen
17	573	42.1	778	6	BD221224	BD221224 Human gen
18	551.6	40.5	559	6	AX385445	AX385445 Sequence
19	535.2	39.3	540	6	AX386014	AX386014 Sequence
20	534.4	39.2	863	6	AX329813	AX329813 Sequence
21	534.4	39.2	863	6	AX330318	AX330318 Sequence
22	534.4	39.2	863	6	AX770551	AX770551 Sequence
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26	321.4	23.6	164746	9	AL732431	AL732431 Human DNA
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31	274	20.1	557	6	AX778681	AX778681 Sequence
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c 42	218.2	16.0	122974	2	AC025114	AC025114 Homo sapi
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45	198	14.5	264558	2	AC135653	AC135653 Rattus no

ALIGNMENTS

RESULT 1
AX301999
LOCUS AX301999 1362 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 3 from Patent WO0174900.
ACCESSION AX301999
VERSION AX301999.1 GI:17382987
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Kaplow,J., Haws,T., Rosier,M. and Denefle,P.
TITLE Nuclear factor kb inducing factor
JOURNAL Patent: WO 0174900-A 3 11-OCT-2001;
Aventis Pharmaceuticals Products Inc. (US)
FEATURES Location/Qualifiers
source 1. .1362
/organism="Homo sapiens"
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/db_xref="taxon:9606"
ORIGIN

Query Match 100.0%; Score 1362; DB 6; Length 1362;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCGCTGGTGCGCGCACTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCCGCTCCGGC 60
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Db          1 ATGGCGCTGGTGCGCGCACTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCCGCTCCGGC 60

Qy         61 CTCGGGCTGCCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTTT 120
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Db         61 CTCGGGCTGCCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTTT 120

Qy        121 TGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAAA 180
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Qy       241 TGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATTCTGGACAA 300
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RESULT 2
BC018999

LOCUS BC018999 1759 bp mRNA linear PRI 29-JUN-2004

DEFINITION Homo sapiens sphingomyelin phosphodiesterase, acid-like 3A, mRNA (cDNA clone MGC:20681 IMAGE:3138813), complete cds.

ACCESSION BC018999

VERSION BC018999.2 GI:33874666

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1759)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED 12477932

REFERENCE 2 (bases 1 to 1759)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov

COMMENT On Aug 19, 2003 this sequence version replaced gi:17512052.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 30 Row: a Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24307910.

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ORIGIN

  Query Match          99.9%;  Score 1360.4;  DB 9;  Length 1759;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1361;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGCGCTGGTGCGCGCACTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCCGCTCCGGC 60
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Qy         61 CTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTTT 120
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Qy        121 TGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAAA 180
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Db        489 CCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGGATCAACTG 548

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Qy        841 AAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTATG 900
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Qy       1021 GATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGCG 1080
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Db       1089 GATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGCG 1148

Qy       1081 AATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACATT 1140
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Db       1149 AATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACATT 1208

Qy       1141 GAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAGT 1200
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Db       1209 GAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAGT 1268

Qy       1201 AAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATGT 1260
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Db       1269 AAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATGT 1328

Qy       1261 GATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTAT 1320
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Db       1329 GATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTAT 1388

Qy       1321 GCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTACTAG 1362
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Db       1389 GCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTACTAG 1430


RESULT 3
AK000184
LOCUS       AK000184                1760 bp    mRNA    linear   PRI 13-SEP-2003
DEFINITION  Homo sapiens cDNA FLJ20177 fis, clone COL09966, highly similar to
            Y08136 H.
ACCESSION   AK000184
VERSION     AK000184.1  GI:7020103
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
            Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
            Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
  TITLE     NEDO human cDNA sequencing project
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JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1760)
AUTHORS Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Deptment of Virology; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).

FEATURES Location/Qualifiers
source 1. .1760
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="COL09966"
/tissue_type="colon"
/clone_lib="COL"
/note="cloning vector pME18SFL3"
misc_feature 1. .1760
/note="highly similar to Y08136 H"

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Query Match 99.9%; Score 1360.4; DB 9; Length 1760;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy    1 ATGGCGCTGGTGCGCGCACTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCCGCTCCGGC 60
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Db   72 ATGGCGCTGGTGCGCGCACTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCCGCTCCGGC 131

Qy   61 CTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTTT 120
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Db  132 CTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTTT 191

Qy  121 TGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAAA 180
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Db  192 TGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAAA 251

Qy  181 GTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGAGATGTTCTG 240
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Qy  241 TGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATTCTGGACAA 300
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Db  492 CCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGGATCAACTG 551

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Db  612 GAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTACAACTAAT 671

Qy  601 CCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAATATAATGACA 660
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Db  672 CCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAATATAATGACA 731

Qy  661 CTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGAACAACTCT 720
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Db  792 CAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATCT 851

Qy  781 TCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCAA 840
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Qy  841 AAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTATG 900
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Qy  901 GTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACA 960
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Db 1092 GATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGCG 1151

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Qy 1141 GAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAGT 1200
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Db 1272 AAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATGT 1331

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RESULT 4
AR113044
LOCUS AR113044 1764 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 13 from patent US 6132964.
ACCESSION AR113044
VERSION AR113044.1 GI:14093366
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1764)
AUTHORS Bandman,O., Lal,P., Hillman,J.L., Corley,N.C., Guegler,K.J. and Shah,P.
TITLE Hydrolase enzymes
JOURNAL Patent: US 6132964-A 13 17-OCT-2000;
FEATURES Location/Qualifiers
source 1. .1764
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

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  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1361;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGCGCTGGTGCGCGCACTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCCGCTCCGGC 60
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Db        609 GAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTACAACTAAT 668

Qy        601 CCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAATATAATGACA 660
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Qy        721 CAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATCT 780
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Qy       1021 GATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGCG 1080
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RESULT 5
AR280051
LOCUS       AR280051                1764 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 13 from patent US 6518029.
ACCESSION   AR280051
VERSION     AR280051.1  GI:29715400
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1764)
  AUTHORS   Bandman,O., Lal,P., Hillman,J.L., Corley,N.C., Guegler,K.J. and
            Shah,P.
  TITLE     Human hydrolase-like molecules
  JOURNAL   Patent: US 6518029-A 13 11-FEB-2003;
FEATURES             Location/Qualifiers
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Db        129 CTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTTT 188

Qy        121 TGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAAA 180
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Qy        181 GTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGAGATGTTCTG 240
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Db        249 GTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGAGATGTTCTG 308

Qy        241 TGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATTCTGGACAA 300
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Db        369 GAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTACCTGAACTC 428
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Qy        361 TCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTTT 420
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Db        729 CTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGAACAACTCT 788

Qy        721 CAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATCT 780
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Db        789 CAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATCT 848

Qy        781 TCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 TCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCAA 908

Qy        841 AAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTATG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        909 AAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTATG 968

Qy        901 GTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 GTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACA 1028

Qy        961 CCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1029 CCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTAT 1088

Qy       1021 GATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGCG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1089 GATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGCG 1148

Qy       1081 AATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACATT 1140
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Db       1149 AATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACATT 1208

Qy       1141 GAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAGT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1209 GAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAGT 1268

Qy       1201 AAGCAGTTTATAAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATGT 1260
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Db       1269 AAGCAGTTTATAAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATGT 1328

Qy       1261 GATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1329 GATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTAT 1388

Qy       1321 GCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTACTAG 1362
              ||||||||||||||||||||||||||||||||||||||||||
Db       1389 GCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTACTAG 1430
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RESULT 6
AX281695
LOCUS AX281695 1746 bp DNA linear PAT 02-NOV-2001

DEFINITION Sequence 104 from Patent WO0177389.
ACCESSION AX281695
VERSION AX281695.1 GI:16608946
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shiffman,D., Somogyi,R., Lawn,R., Seilhamer,J.J., Porter,G.J.,
Mikita,T. and Tai,J.
TITLE Genes expressed in foam cell differentiation
JOURNAL Patent: WO 0177389-A 104 18-OCT-2001;
Incyte Genomics, Inc. (US)
FEATURES Location/Qualifiers
source 1. .1746
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 233778.9"
ORIGIN

Query Match 99.1%; Score 1349.4; DB 6; Length 1746;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1361; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy          1 ATGGCGCTGGTGCGCGCAC-TCGTCTGCTGCCTGCTGACTGCCTGGCACTGCCGCTCCGG 59
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         69 ATGGCGCTGGTGCGCGCACTTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCCGCTCCGG 128

Qy         60 CCTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTT 119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 CCTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTT 188

Qy        120 TTGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAA 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 TTGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAA 248

Qy        180 AGTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGAGATGTTCT 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AGTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGAGATGTTCT 308

Qy        240 GTGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATTCTGGACA 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 GTGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATTCTGGACA 368

Qy        300 AGAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTACCTGAACT 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 AGAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTACCTGAACT 428

Qy        360 CTCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTT 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 CTCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTT 488

Qy        420 TCCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGGATCAACT 479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 TCCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGGATCAACT 548

Qy        480 GTCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCATGGCTAGA 539
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Db        549 GCCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCATGGCTAGA 608

Qy        540 TGAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTACAACTAA 599
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Db        609 TGAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTACAACTAA 668

Qy        600 TCCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAATATAATGAC 659
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 TCCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAATATAATGAC 728

Qy        660 ACTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGAACAACTC 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 ACTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGAACAACTC 788
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Qy       720 TCAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATC 779
Db       789 TCAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATC 848

Qy       780 TTCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCA 839
Db       849 TTCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCA 908

Qy       840 AAAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTAT 899
Db       909 AAAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTAT 968

Qy       900 GGTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTAC 959
Db       969 GGTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTAC 1028

Qy       960 ACCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTA 1019
Db      1029 ACCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTA 1088

Qy      1020 TGATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGC 1079
Db      1089 TGATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGC 1148

Qy      1080 GAATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACAT 1139
Db      1149 GAATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACAT 1208

Qy      1140 TGAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAG 1199
Db      1209 TGAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAG 1268

Qy      1200 TAAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATG 1259
Db      1269 TAAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATG 1328

Qy      1260 TGATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTA 1319
Db      1329 TGATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTA 1388

Qy      1320 TGCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTACTAG 1362
Db      1389 TGCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTACTAG 1431
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RESULT 7
AX780232
LOCUS       AX780232                2505 bp    DNA     linear   PAT 14-JUL-2003
DEFINITION  Sequence 2389 from Patent WO03039443.
ACCESSION   AX780232
VERSION     AX780232.1  GI:32697226
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Haferlach,T., Schoch,C., Kern,W., Kohlmann,A., Schnittger,S.,
            Dugas,M., Eils,R., Brors,B. and Mergenthaler,S.
  TITLE     Novel genetic markers for leukemias
  JOURNAL   Patent: WO 03039443-A 2389 15-MAY-2003;
            Deutsches Krebsforschungszentrum (DE) ;
            Ludwig-Maximilian-Universitaet Muenchen (DE) ; Haferlach, Torsten,
            PD Dr. Dr. (DE) ; Schoch, Claudia (DE) ; Kern, Wolfgang (DE)
FEATURES             Location/Qualifiers
     source          1. .2505
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             98.5%;  Score 1341.4;  DB 6;  Length 2505;
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  Best Local Similarity   99.3%;  Pred. No. 0;
  Matches 1353;  Conservative    0;  Mismatches    9;  Indels    1;  Gaps    1;

Qy         1 ATGGCGCTGGTGCGCGCACTCGTCTGCTGCC-TGCTGACTGCCTGGCACTGCCGCTCCGG 59
Db       590 ATGGCGCTGGTGCGCGCACTCGTCTGCTGCCNTGCTGACTGCCTGGCACTGCCGCTCCGG 649

Qy        60 CCTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTT 119
Db       650 CCTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGNNAGTT 709

Qy       120 TTGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAA 179
Db       710 NTNNNATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAA 769

Qy       180 AGTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGAGATGTTCT 239
Db       770 AGTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTNTGGAGATGTTCT 829

Qy       240 GTGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATTCTGGACA 299
Db       830 GTGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATTCTGGACA 889

Qy       300 AGAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTACCTGAACT 359
Db       890 AGAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTACCTGAACT 949

Qy       360 CTCAACAGACACTGTTATAAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTT 419
Db       950 CTCAACAGACACTGTTATAAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTT 1009

Qy       420 TCCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGGATCAACT 479
Db      1010 TCCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGGATCAACT 1069

Qy       480 GTCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCATGGCTAGA 539
Db      1070 GCCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCATGGCTAGA 1129

Qy       540 TGAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTACAACTAA 599
Db      1130 TGAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTACAACTAA 1189

Qy       600 TCCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAATATAATGAC 659
Db      1190 TCCAAACCTTAGGATCATCAGTCTANACACAAACTTGTACTACGGCCCAAATATAATGAC 1249

Qy       660 ACTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGAACAACTC 719
Db      1250 ACTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGAACAACTC 1309

Qy       720 TCAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATC 779
Db      1310 TCAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATC 1369

Qy       780 TTCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCA 839
Db      1370 TTCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCA 1429

Qy       840 AAAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTAT 899
Db      1430 AAAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTAT 1489

Qy       900 GGTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTAC 959
Db      1490 GGTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTAC 1549

Qy       960 ACCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTA 1019
Db      1550 ACCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTA 1609

Qy      1020 TGATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGC 1079
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Db       1610 TGATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGC 1669

Qy       1080 GAATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACAT 1139
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Db       1670 GAATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACAT 1729

Qy       1140 TGAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAG 1199
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1730 TGAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAG 1789

Qy       1200 TAAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATG 1259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1790 TAAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATG 1849

Qy       1260 TGATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTA 1319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1850 TGATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTA 1909

Qy       1320 TGCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTACTAG 1362
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Db       1910 TGCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTACTAG 1952


RESULT 8
CQ414095
LOCUS       CQ414095                2049 bp    DNA     linear   PAT 23-JAN-2004
DEFINITION  Sequence 21166 from Patent WO0170979.
ACCESSION   CQ414095
VERSION     CQ414095.1  GI:41321876
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lee,J. and Lillie,J.
  TITLE     Genes, compositions, kits, and method for identification,
            assessment, prevention, and therapy of ovarian cancer
  JOURNAL   Patent: WO 0170979-A 21166 27-SEP-2001;
            Millennium Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .2049
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             76.0%;  Score 1035.4;  DB 6;  Length 2049;
  Best Local Similarity   99.9%;  Pred. No. 1.5e-246;
  Matches 1036;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        326 GGGATAGCCCACCTCATGTTCCTGTACCTGAACTCTCAACAGACACTGTTATAAATGTGA 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 GGGATAGCCCACCTCATGTTCCTGTACCTGAACTCTCAACAGACACTGTTATAAATGTGA 269

Qy        386 TCACTAATATGACAACCACCATCCAGAGTCTCTTTCCAAATCTCCAGGTTTTCCCTGCGC 445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 TCACTAATATGACAACCACCATCCAGAGTCTCTTTCCAAATCTCCAGGTTTTCCCTGCGC 329

Qy        446 TGGGTAATCATGACTATTGGCCACAGGATCAACTGTCTGTAGTCACCAGTAAAGTGTACA 505
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        330 TGGGTAATCATGACTATTGGCCACAGGATCAACTGCCTGTAGTCACCAGTAAAGTGTACA 389

Qy        506 ATGCAGTAGCAAACCTCTGGAAACCATGGCTAGATGAAGAAGCTATTAGTACTTTAAGGA 565
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 ATGCAGTAGCAAACCTCTGGAAACCATGGCTAGATGAAGAAGCTATTAGTACTTTAAGGA 449

Qy        566 AAGGTGGTTTTTATTCACAGAAAGTTACAACTAATCCAAACCTTAGGATCATCAGTCTAA 625
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 AAGGTGGTTTTTATTCACAGAAAGTTACAACTAATCCAAACCTTAGGATCATCAGTCTAA 509

Qy        626 ACACAAACTTGTACTACGGCCCAAATATAATGACACTGAACAAGACTGACCCAGCCAACC 685
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        510 ACACAAACTTGTACTACGGCCCAAATATAATGACACTGAACAAGACTGACCCAGCCAACC 569

Qy        686 AGTTTGAATGGCTAGAAAGTACATTGAACAACTCTCAGCAGAATAAGGAGAAGGTGTATA 745
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        570 AGTTTGAATGGCTAGAAAGTACATTGAACAACTCTCAGCAGAATAAGGAGAAGGTGTATA 629

Qy        746 TCATAGCACATGTTCCAGTGGGGTATCTGCCATCTTCACAGAACATCACAGCAATGAGAG 805
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Db        630 TCATAGCACATGTTCCAGTGGGGTATCTGCCATCTTCACAGAACATCACAGCAATGAGAG 689

Qy        806 AATACTATAATGAGAAATTGATAGATATTTTTCAAAAATACAGTGATGTCATTGCAGGAC 865
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Db        690 AATACTATAATGAGAAATTGATAGATATTTTTCAAAAATACAGTGATGTCATTGCAGGAC 749

Qy        866 AATTTTATGGACACACTCACAGAGACAGCATTATGGTTCTTTCAGATAAAAAAGGAAGTC 925
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Db        750 AATTTTATGGACACACTCACAGAGACAGCATTATGGTTCTTTCAGATAAAAAAGGAAGTC 809

Qy        926 CAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACACCAGTGAAGAGTGTTTTAGAAAAAC 985
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Db        810 CAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACACCAGTGAAGAGTGTTTTAGAAAAAC 869

Qy        986 AGACCAACAATCCTGGTATCAGACTGTTTCAGTATGATCCTCGTGATTATAAATTATTGG 1045
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Db        870 AGACCAACAATCCTGGTATCAGACTGTTTCAGTATGATCCTCGTGATTATAAATTATTGG 929

Qy       1046 ATATGTTGCAGTATTACTTGAATCTGACAGAGGCGAATCTAAAGGGAGAGTCCATCTGGA 1105
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Db        930 ATATGTTGCAGTATTACTTGAATCTGACAGAGGCGAATCTAAAGGGAGAGTCCATCTGGA 989

Qy       1106 AGCTGGAGTATATCCTGACCCAGACCTACGACATTGAAGATTTGCAGCCGGAAAGTTTAT 1165
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Db        990 AGCTGGAGTATATCCTGACCCAGACCTACGACATTGAAGATTTGCAGCCGGAAAGTTTAT 1049

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Qy       1226 ACTTCTTTGTGAGTTATGACAGCAGTGTAACATGTGATAAGACATGTAAGGCCTTTCAGA 1285
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Db       1110 ACTTCTTTGTGAGTTATGACAGCAGTGTAACATGTGATAAGACATGTAAGGCCTTTCAGA 1169

Qy       1286 TTTGTGCAATTATGAATCTTGATAATATTTCCTATGCAGATTGCCTCAAACAGCTTTATA 1345
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Db       1170 TTTGTGCAATTATGAATCTTGATAATATTTCCTATGCAGATTGCCTCAAACAGCTTTATA 1229

Qy       1346 TAAAGCACAATTACTAG 1362
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Db       1230 TAAAGCACAATTACTAG 1246


RESULT 9
AX305693
LOCUS       AX305693                1758 bp    DNA     linear   PAT 11-DEC-2001
DEFINITION  Sequence 444 from Patent WO0188188.
ACCESSION   AX305693
VERSION     AX305693.1  GI:17645124
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Ishikawa,K., Asai,S., Takahashi,Y., Nagata,T. and Ishii,Y.
  TITLE     Method for examining ischemic conditions
  JOURNAL   Patent: WO 0188188-A 444 22-NOV-2001;
            School Juridical Person Nihon University (JP)
FEATURES             Location/Qualifiers
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ORIGIN
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  Matches 1115;  Conservative    1;  Mismatches  236;  Indels   10;  Gaps    2;

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RESULT 10
MMASML3A
LOCUS       MMASML3A                1758 bp    mRNA    linear   ROD 19-SEP-1996
DEFINITION  M.musculus mRNA for ASM-like phosphodiesterase 3a.
ACCESSION   Y08135
VERSION     Y08135.1  GI:1552349
KEYWORDS    acid sphingomyelinase; ASML3 gene; phosphodiesterase.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Hofmann,K.
  TITLE     Acid Sphingomyelinase is a member of a multi-gene family and shares
            motifs with a large family of metallo-phosphoesterases
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1758)
  AUTHORS   Hofmann,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-SEP-1996) K. Hofmann, Isrec (Swiss Inst. F. Exp.
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ORIGIN
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Query Match             69.4%;  Score 944.6;  DB 10;  Length 1758;
Best Local Similarity   81.9%;  Pred. No. 5.8e-224;
Matches 1115;  Conservative    1;  Mismatches  236;  Indels   10;  Gaps    2;

Qy          1 ATGGCGCTGGTGCGCGCACTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCCGCTCCGGC 60
              |||||| || || ||    || | ||||||| ||| |||||||| |||| || | ||
Db         93 ATGGCGTTGCTGGGCAACTTCCTTTGCTGCCTACTGGTTGCCTGGCTCTGCGGCCCGGGG 152

Qy         61 CTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTTT 120
              |||||| ||||| ||||||| ||          | |||   | || ||  | || |||||||
Db        153 CTCGGGGTGCCCCTGGCGCCGGC---------GGATCGCGCCCCAGCTGTGGGGCAGTTT 203

Qy        121 TGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAAA 180
              ||||| |||||||||||||||  |||||||||||||||||||| |||||||||  || ||
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Qy        181 GTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGAGATGTTCTG 240
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Qy        241 TGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATTCTGGACAA 300
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Db        324 TGTGACTCTCCATATCAACTTATTTTGTCAGCCTTTGATTTTATTAAGAATTCAGGACAA 383

Qy        301 GAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTACCTGAACTC 360
              |||||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Db        384 GAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTGCCAGTACCTGAACTC 443

Qy        361 TCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTTT 420
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Db        564 CCAATAGTCACCAGTAAGGTCTACAGTGCTGTGGCTGACCTCTGGAAACCCTGGCTGGGT 623

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Db        624 GAAGAAGCTATTAGCACTTTAAAGAAAGGTGGTTTTTACTCACAGAAAGTTGCAAGTAAT 683

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              |||  | | |||||||| || |||||||||||||||||||| |||||||| || |||||
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Db        744 CTGAACAAGACAGACCCAGCAAATCAGTTTGAATGGCTGGAAAATACACTCAACAGCTCT 803

Qy        721 CAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATCT 780
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Db        804 CTATGGAATAAGGAGAAGGTATACMTCATAGCGCATGTTCCAGTGGGCTATCTCCCTTAT 863

Qy        781 TCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCAA 840
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RESULT 11
BC082029
LOCUS       BC082029                1706 bp    mRNA    linear   ROD 12-OCT-2004
DEFINITION  Rattus norvegicus acid sphingomyelinase-like phosphodiesterase 3A,
            mRNA (cDNA clone MGC:95161 IMAGE:7130096), complete cds.
ACCESSION   BC082029
VERSION     BC082029.1  GI:51980328
KEYWORDS    MGC.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 1706)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
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            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
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            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1706)
  AUTHORS   Director MGC Project.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Howard Jacobs
            cDNA Library Preparation: Express Genomics
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
```

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 184 Row: g Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

FEATURES Location/Qualifiers

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ORIGIN

Query Match 68.8%; Score 936.4; DB 10; Length 1706;
Best Local Similarity 81.6%; Pred. No. 6.4e-222;
Matches 1111; Conservative 0; Mismatches 241; Indels 10; Gaps 2;

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Qy  361 TCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTTT 420
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Qy  481 TCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCATGGCTAGAT 540
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Qy  541 GAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTACAACTAAT 600
Db  546 GAAGAAGCTATTAGCACTTTAAGGAAAGGTGGTTTTTACTCACAGAAAGTTGCAAGTAAT 605

Qy  601 CCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAATATAATGACA 660
Db  606 CCAGACTTGAGGATCATTAGCCTAAACACAAACTTGTACTATGGCCCAAATATCATGACC 665

Qy  661 CTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGAACAACTCT 720
Db  666 CTGAACAAGACAGACCCAGCAAATCAGTTTGAATGGCTGGAAAATACACTCAACAGCTCT 725

Qy  721 CAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATCT 780
Db  726 CTGCGAAATAAGGAGAAGGTATACGTCATAGCACATGTGCCAGTGGGCTATCTCCCTTAT 785

Qy  781 TCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCAA 840
Db  786 GCAACCAAGACCCCAGCAATGAGGCAGTACTATAATGAGAAACTGGTTGATATTTTCAGA 845

Qy  841 AAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTATG 900
Db  846 AGATACAGCTCCGTTATTGCCGGACAGTTCTATGGCCACACCCATAGAGACAGCCTTATG 905

Qy  901 GTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACA 960
Db  906 GTCCTTTCAGATAAAAACGGTAATCCAATAAATTCTGTGTTTGTGGCACCTGCTGTTACA 965

Qy  961 CCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTAT 1020
Db  966 CCAGTGAAAGGAGTTTTAGAAAAAGAGACCAACAATCCTGGCGTCCGTCTGTTTCAGTAC 1025

Qy 1021 GATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGCG 1080
Db 1026 AAGCCTGGTGATTACACACTGCTGGACATGTTGCAGTATTACTTGAACTTGACAGAAGCC 1085

Qy 1081 AATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACATT 1140
Db 1086 AATCTAAAAGGAGAATCCAATTGGACCCTGGAGTACACCTTGACTCAGGCCTATGGTGTC 1145

Qy 1141 GAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAGT 1200
Db 1146 GCAGACCTGCAGCCAAAGAGCTTACATGGATTAGCTCAGCAGCTTGCTACCATAGACAGC 1205

Qy 1201 AAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATGT 1260
Db 1206 AAGCAGTTCCTGAAATACTACCATTATTTTTTTGTGAGTTATGACAGCAGCGCACCTTGT 1265

Qy 1261 GATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTAT 1320
Db 1266 GATCAACGATGTAAGACCTTACAGATATGTGCAATTATGAATCTTGACCTTGTTTCCTAT 1325

Qy 1321 GCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTACTAG 1362
Db 1326 GAGGATTGCCTTAAACGACATT-TATAAAGCATAGTCACTGG 1366
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RESULT 12
AX302000
LOCUS AX302000 1095 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 4 from Patent WO0174900.
ACCESSION AX302000
VERSION AX302000.1 GI:17382988

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KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kaplow,J., Haws,T., Rosier,M. and Denefle,P.
  TITLE     Nuclear factor kb inducing factor
  JOURNAL   Patent: WO 0174900-A 4 11-OCT-2001;
            Aventis Pharmaceuticals Products Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1095
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             59.9%;  Score 816.4;  DB 6;  Length 1095;
  Best Local Similarity   80.3%;  Pred. No. 4.5e-192;
  Matches 1094;  Conservative    0;  Mismatches    1;  Indels  267;  Gaps    1;

Qy          1 ATGGCGCTGGTGCGCGCACTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCCGCTCCGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCGCTGGTGCGCGCACTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCCGCTCCGGC 60

Qy         61 CTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTTT 120

Qy        121 TGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAAA 180
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Db        121 TGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAAA 180

Qy        181 GTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGAGATGTTCTG 240
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Db        181 GTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGAGATGTTCTG 240

Qy        241 TGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATTCTGGACAA 300
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Db        241 TGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATTCTGGACAA 300

Qy        301 GAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTACCTGAACTC 360
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Db        301 GAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTACCTGAACTC 360

Qy        361 TCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTTT 420
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Db        361 TCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTTT 420

Qy        421 CCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGGATCAACTG 480
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Db        421 CCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCAC---------- 469

Qy        481 TCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCATGGCTAGAT 540

Db        470 ---------------------------------------------------------- 469

Qy        541 GAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTACAACTAAT 600

Db        470 ---------------------------------------------------------- 469

Qy        601 CCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAATATAATGACA 660

Db        470 ---------------------------------------------------------- 469

Qy        661 CTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGAACAACTCT 720

Db        470 ---------------------------------------------------------- 469

Qy        721 CAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATCT 780
                          ||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 ----------------AGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATCT 513

Qy        781 TCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 TCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCAA 573

Qy        841 AAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTATG 900
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Db        574 AAGTACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTATG 633

Qy        901 GTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACA 693

Qy        961 CCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 CCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTAT 753

Qy       1021 GATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGCG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 GATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGCG 813

Qy       1081 AATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 AATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACATT 873

Qy       1141 GAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAGT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 GAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAGT 933

Qy       1201 AAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATGT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 AAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATGT 993

Qy       1261 GATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 GATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTAT 1053

Qy       1321 GCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTACTAG 1362
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Db       1054 GCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTACTAG 1095


RESULT 13
CQ717782
LOCUS       CQ717782                 893 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 3716 from Patent WO02068579.
ACCESSION   CQ717782
VERSION     CQ717782.1  GI:42278639
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 3716 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .893
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             52.7%;  Score 717.4;  DB 6;  Length 893;
  Best Local Similarity   99.9%;  Pred. No. 1.9e-167;
  Matches  718;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        326 GGGATAGCCCACCTCATGTTCCTGTACCTGAACTCTCAACAGACACTGTTATAAATGTGA 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 GGGATAGCCCACCTCATGTTCCTGTACCTGAACTCTCAACAGACACTGTTATAAATGTGA 234
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Qy        386 TCACTAATATGACAACCACCATCCAGAGTCTCTTTCCAAATCTCCAGGTTTTCCCTGCGC 445
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Db        235 TCACTAATATGACAACCACCATCCAGAGTCTCTTTCCAAATCTCCAGGTTTTCCCTGCGC 294

Qy        446 TGGGTAATCATGACTATTGGCCACAGGATCAACTGTCTGTAGTCACCAGTAAAGTGTACA 505
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        295 TGGGTAATCATGACTATTGGCCACAGGATCAACTGCCTGTAGTCACCAGTAAAGTGTACA 354

Qy        506 ATGCAGTAGCAAACCTCTGGAAACCATGGCTAGATGAAGAAGCTATTAGTACTTTAAGGA 565
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Db        355 ATGCAGTAGCAAACCTCTGGAAACCATGGCTAGATGAAGAAGCTATTAGTACTTTAAGGA 414

Qy        566 AAGGTGGTTTTTTATTCACAGAAAGTTACAACTAATCCAAACCTTAGGATCATCAGTCTAA 625
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 AAGGTGGTTTTTTATTCACAGAAAGTTACAACTAATCCAAACCTTAGGATCATCAGTCTAA 474

Qy        626 ACACAAACTTGTACTACGGCCCAAATATAATGACACTGAACAAGACTGACCCAGCCAACC 685
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 ACACAAACTTGTACTACGGCCCAAATATAATGACACTGAACAAGACTGACCCAGCCAACC 534

Qy        686 AGTTTGAATGGCTAGAAAGTACATTGAACAACTCTCAGCAGAATAAGGAGAAGGTGTATA 745
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Db        535 AGTTTGAATGGCTAGAAAGTACATTGAACAACTCTCAGCAGAATAAGGAGAAGGTGTATA 594

Qy        746 TCATAGCACATGTTCCAGTGGGGTATCTGCCATCTTCACAGAACATCACAGCAATGAGAG 805
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Db        595 TCATAGCACATGTTCCAGTGGGGTATCTGCCATCTTCACAGAACATCACAGCAATGAGAG 654

Qy        806 AATACTATAATGAGAAATTGATAGATATTTTTCAAAAATACAGTGATGTCATTGCAGGAC 865
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 AATACTATAATGAGAAATTGATAGATATTTTTCAAAAATACAGTGATGTCATTGCAGGAC 714

Qy        866 AATTTTATGGACACACTCACAGAGACAGCATTATGGTTCTTTCAGATAAAAAAGGAAGTC 925
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 AATTTTATGGACACACTCACAGAGACAGCATTATGGTTCTTTCAGATAAAAAAGGAAGTC 774

Qy        926 CAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACACCAGTGAAGAGTGTTTTAGAAAAAC 985
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Db        775 CAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACACCAGTGAAGAGTGTTTTAGAAAAAC 834

Qy        986 AGACCAACAATCCTGGTATCAGACTGTTTCAGTATGATCCTCGTGATTATAAATTATTG 1044
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 AGACCAACAATCCTGGTATCAGACTGTTTCAGTATGATCCTCGTGATTATAAATTATTG 893
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RESULT 14
BD221252
LOCUS BD221252 728 bp DNA linear PAT 17-JUL-2003
DEFINITION Human gene and gene expression product V.
ACCESSION BD221252
VERSION BD221252.1 GI:33031022
KEYWORDS JP 2002534055-A/2365.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 728)
AUTHORS Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Klinger,J.S., Reinhard,C., Giese,K., Randazzo,F., Kennedy,G.C., Pot,D., Kassam,A., Lamson,G., Drmanac,R., Crkvenjakov,R., Dickson,M., Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V., Jones,L.W. and Crain,B.S.
TITLE Human gene and gene expression product V
JOURNAL Patent: JP 2002534055-A 2365 15-OCT-2002;
CHIRON CORP,HYSEQ INC
COMMENT OS Homo sapiens (human)
PN JP 2002534055-A/2365
PD 15-OCT-2002
PF 13-MAY-1999 JP 2000548466
PR 14-MAY-1998 US 60/085426,15-MAY-1998 US 60/085537 PR
15-MAY-1998 US 60/085696,21-OCT-1998 US 60/105234 PR
27-OCT-1998 US 60/105877
PI LOUIS T WILLIAMS,JAIME ESCOBEDO,MICHAEL A INNIS,PABLO PI DOMINGUEZ GARCIA,
PI JULIE SUDDUTH KLINGER,CHRISTOPH REINHARD,KLAUSE GIESE,FILIPPO PI RANDAZZO,
PI GIULIA C KENNEDY,DAVID POT,ALTAF KASSAM,GEORGE LAMSON,RADOJE PI DRMANAC,
PI RADOMIR CRKVENJAKOV,MARK DICKSON,SNEZANA DRMANAC,IVAN LABAT, PI DENA LESHKOWITZ,DAVID KITA,VERONICA GARCIA,LEE WILLIAM JONES, PI BIRGIT STACHE CRAIN
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC ,C12N5/00,C12Q1/68,
PC C12N15/00,C12N5/00
CC n = A,T,C or G
FH Key Location/Qualifiers
FT misc_feature (1). .(728).

FEATURES Location/Qualifiers
source 1. .728
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ORIGIN

Query Match 51.4%; Score 700.2; DB 6; Length 728;
Best Local Similarity 98.7%; Pred. No. 3.5e-163;
Matches 705; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy        315 GATATGGACAGGGGATAGCCCACCTCATGTTCCTGTACCTGAACTCTCAACAGACACTGT 374
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Db         15 GATTCGGCACGAGGATAGCCCACCTCATGTTCCTGTACCTGAACTCTCAACAGACACTGT 74

Qy        375 TATAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTTTCCAAATCTCCAGGT 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         75 TATAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTTTCCAAATCTCCAGGT 134

Qy        435 TTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGGATCAACTGTCTGTAGTCACCAG 494
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Db        135 TTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGGATCAACTGCCTGTAGTCACCAG 194

Qy        495 TAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCATGGCTAGATGAAGAAGCTATTAG 554
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Db        195 TAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCATGGCTAGATGAAGAAGCTATTAG 254

Qy        555 TACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTACAACTAATCCAAACCTTAGGAT 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 TACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTACAACTAATCCAAACCTTAGGAT 314

Qy        615 CATCAGTCTAAACACAAACTTGTACTACGGCCCAAATATAATGACACTGAACAAGACTGA 674
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Db        315 CATCAGTCTAAACACAAACTTGTACTACGGCCCAAATATAATGACACTGAACAAGACTGA 374

Qy        675 CCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGAACAACTCTCAGCAGAATAAGGA 734
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Db        375 CCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGAACAACTCTCAGCAGAATAAGGA 434

Qy        735 GAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATCTTCACAGAACATCAC 794
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Db        435 GAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATCTTCACAGAACATCAC 494

Qy        795 AGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCAAAAATACAGTGATGT 854
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Db        495 AGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCAAAAATACAGTGATGT 554

Qy        855 CATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTATGGTTCTTTCAGATAA 914
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Db        555 CATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTATGGTTCTTTCAGATAA 614

Qy        915 AAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACACCAGTGAAGAGTGT 974
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Db        615 AAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACACCAGTGAAGAGTGT 674

Qy        975 TTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTATGATCCTCG 1028
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Db        675 TTTAGAAAAACAGACCAACAATNCTGGTATCAGACTGGTTCAGTATGATCCTCG 728
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RESULT 15
AJ719446
LOCUS AJ719446 2842 bp mRNA linear VRT 30-SEP-2004
DEFINITION Gallus gallus mRNA for hypothetical protein, clone 2h6.
ACCESSION AJ719446
VERSION AJ719446.1 GI:53127443
KEYWORDS ORF1.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1
AUTHORS Caldwell,R.B., Kierzek,A.M., Arakawa,H., Bezzubov,Y., Zaim,J., Fiedler,P., Kutter,S., Blagodatski,A., Kostovska,D., Koter,M., Plachy,J., Carninci,P., Hayashizaki,Y. and Buerstedde,J.M.
TITLE Full-length cDNAs from bursal lymphocytes to facilitate gene function analysis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2842)
AUTHORS Caldwell,R.B.
TITLE Direct Submission
JOURNAL Submitted (20-MAY-2004) Caldwell R.B., GSF - Forschungszentrum, Institut fuer Molekulare Strahlenbiologie, Ingolstaedter Landstr. 1, D-85764 Neuherberg, GERMANY
FEATURES Location/Qualifiers
source 1. .2842
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/db_xref="taxon:9031"
/clone="2h6"
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/dev_stage="2 weeks old"
gene 1. .2842
/locus_tag="RCJMB04_2h6"
5'UTR <1. .110
/locus_tag="RCJMB04_2h6"
CDS 111. .263
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/note="ORF1"
/codon_start=1
/product="hypothetical protein"
/protein_id="CAG31105.1"
/db_xref="GI:53127444"
/translation="MEPPGGRAARLALVAAWRCSALHCELPRRRRPARCPALLWGSFG IYLICT"
3'UTR 264. .>2842
/locus_tag="RCJMB04_2h6"
ORIGIN

Query Match 50.6%; Score 689; DB 5; Length 2842;
Best Local Similarity 71.2%; Pred. No. 2.5e-160;
Matches 924; Conservative 0; Mismatches 364; Indels 9; Gaps 1;

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Qy         51 CCGCTCCGGCCTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGAT 110
Db        169 CTGCTCTGCACTGCGAGCTGCCGCGGCGGCGCCGGCCGGCCCGGTGCCCCGCTCTGCTGT 228

Qy        111 AGGACAGTTTTGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGA 170
Db        229 GGGGCAGTTTTGGCATATATCTGATCTGCACTTAGATCCAACTTACCACATCACTCCTGA 288

Qy        171 CCACACAAAAGTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGG 230
Db        289 TCACACCAAAGTTTGTTCTTCTTCCAAAGGAGCCAATGCCTCTAACCCAGGCCCTTTTGG 348

Qy        231 AGATGTTCTGTGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAA 290
Db        349 AGACTTTTTATGTGATTCTCCATATGAACTTATTTTGTCAGCATTTACATTCATGAAGGA 408

Qy        291 TTCTGGACAAGAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGT 350
Db        409 TTCAAAACAGCAGGCGTCATTCATGATTTGGACAGGAGATAGCCCTCCTCATGTTCCAGT 468

Qy        351 ACCTGAACTCTCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCA 410
Db        469 GGAAGAACTCTCCACAAAGTTGGTCATTAATATCATTGGCAATATGAGTTCTACAATTCA 528

Qy        411 GAGTCTCTTTCCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACA 470
Db        529 TAGTTTCTTTCCAGATCTTCAGGTTTTTCCAGCCTTGGGAAATCATGATTACTGGCCACA 588

Qy        471 GGATCAACTGTCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACC 530
Db        589 GGATCAGCTTCCTGTAACCACCAGTGAAGTTTACAATGCTGTAGCAGATTTCTGGAAGCC 648

Qy        531 ATGGCTAGATGAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGT 590
Db        649 TTGGCTAACTGATGAAGCCATCAGTACCTTCAGAAAAGGTGGCTTTTACACACAACTGTT 708

Qy        591 TACAACTAATCCAAAC---------CTTAGGATCATCAGTCTAAACACAAACTTGTACTA 641
Db        709 TGAATCGAATGTGAGCTCTGAACCTCTCAGGATAATCAGTTTGAACACAAATTTGTATTA 768

Qy        642 CGGCCCAAATATAATGACACTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGA 701
Db        769 CAGCCCAAACCACGTGACTGTGAATATCACAGACCCAGCCAACCAGTTGGCCTGGCTGGA 828

Qy        702 AAGTACATTGAACAACTCTCAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCC 761
Db        829 GGGAATACTAGAAGCCTCTTCACAAAAGAAGGAAAAGGTATATGTAATAGGACATGTACC 888

Qy        762 AGTGGGGTATCTGCCATCTTCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAA 821
Db        889 AATAGGATACTTGCCATTTGCAAGGAATACTACAGCTATCAGAGAATATTACAATGAGAG 948

Qy        822 ATTGATAGATATTTTTCAAAAATACAGTGATGTCATTGCAGGACAATTTTATGGACACAC 881
Db        949 ACTGGTAAAAATTTTTCGCAAATATAGTAGTGTTATTGCTGGGCAATTTTTTGGACACAC 1008

Qy        882 TCACAGAGACAGCATTATGGTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTT 941
Db       1009 ACATAGAGACAGTATCATGGTCCTCCTGGATGAAGAAGAAAAGCCAGTCAATTCCTTGTT 1068

Qy        942 TGTGGCTCCTGCTGTTACACCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGG 1001
Db       1069 TGTGGCACCTGCTGTGACCCCAGTGAAGAATGTATGGCAAATGGAATCCAATAACCCAGG 1128

Qy       1002 TATCAGACTGTTTCAGTATGATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTA 1061
Db       1129 TGTCAGATTGTATCAATATGATCCCCTTAATTATAGCTTGCTGGATCTTTGGCAGTTTTA 1188

Qy       1062 CTTGAATCTGACAGAGGCGAATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCT 1121
Db       1189 CTTGGACCTCAGAGATGCTAACAAGAAAAATGAATCAAACTGGAAATTAGAATACATCTT 1248

Qy       1122 GACCCAGACCTACGACATTGAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACA 1181
Db       1249 GACTAAAGCTTATGGCATTGAAGATTTGAAGCCAGAAAGTTTATATGAAATGGCCAAGCA 1308

Qy       1182 ATTTACAATCCTAGACAGTAAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTA 1241
Db       1309 GTTGTCTGTGCCACATAGCACACTGTTTGAGCAGTATTACAATAACTTCATTGTGAGTTA 1368

Qy       1242 TGACAGCAGTGTAACATGTGATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAA 1301
Db       1369 TAACAAAACCATTGTCTGTGAAGAGGGGTGCAAGACCTGCCAAATATGTGCAATCCAATA 1428

Qy       1302 TCTTGATAATATTTCCTATGCAGATTGCCTCAAACAG 1338
Db       1429 TCTGGATTATTCCTCATACACAGATTGTATCAATCGG 1465
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Search completed: April 5, 2005, 09:16:57
Job time : 5850 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 5, 2005, 10:08:58 ; Search time 628 Seconds
(without alignments)
4270.132 Million cell updates/sec

Title: US-09-823-119B-1
Perfect score: 2427
Sequence: 1 MALVRALVCCLLTAWHCRSG.....NLDNISYADCLKQLYIKHNY 453

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09823119/runat_05042005_084015_6991/app_query.fasta_1.647
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2427	100.0	1362	4	AAD21343	Aad21343 Human nuc
2	2422	99.8	1763	10	ADH61155	Adh61155 Human hyd
3	2422	99.8	1764	4	AAC60227	Aac60227 Human hyd
4	2422	99.8	1764	9	ADA10929	Ada10929 Human cDN
5	2422	99.8	1764	10	ADB90834	Adb90834 Human cDN
6	2422	99.8	1768	12	ADJ45508	Adj45508 cDNA enco
7	2413	99.4	1783	6	AAS62765	Aas62765 cDNA sequ
8	2409	99.3	1746	6	AAS94849	Aas94849 Human DNA
9	2355	97.0	2505	10	ADF81833	Adf81833 Leukaemia
10	2223	91.6	1873	4	AAI61110	Aai61110 Human pol
11	2223	91.6	1874	4	AAI59324	Aai59324 Human pol
12	1962.5	80.9	2049	5	ADL62954	Adl62954 Human ova
13	1953.5	80.5	1758	6	ABI99482	Abi99482 Mouse isc
14	1903.5	78.4	1095	4	AAD21344	Aad21344 Human nuc
15	1209	49.8	728	3	AAA02374	Aaa02374 Human col
16	1162	47.9	733	3	AAA02333	Aaa02333 Human col
17	1101	45.4	939	5	AAH20423	Aah20423 Human sph
18	1004	41.4	559	6	ABN60406	Abn60406 Human can
19	986.5	40.6	778	3	AAA02346	Aaa02346 Human col
20	956	39.4	773	3	AAA02332	Aaa02332 Human col
21	932	38.4	540	6	ABN60975	Abn60975 Human can
22	930	38.3	863	6	ABL62490	Abl62490 Colon ade
23	930	38.3	863	6	ABL61985	Abl61985 Colon ade
24	930	38.3	863	6	ABK84743	Abk84743 Human cDN
25	930	38.3	863	8	ACA89936	Aca89936 Gene diff
26	930	38.3	863	10	ADH28998	Adh28998 Human chr
27	930	38.3	863	13	ADP24656	Adp24656 PRO polyp
28	921	37.9	1489	4	AAH99916	Aah99916 Nucleotid
29	921	37.9	1814	4	AAI59259	Aai59259 Human pol
C 30	921	37.9	1816	4	AAI61045	Aai61045 Human pol
31	917	37.8	1610	6	ABL68027	Abl68027 Ovary can
32	917	37.8	1610	6	ABL64782	Abl64782 Lung canc
33	878	36.2	610	10	ADB90860	Adb90860 Human hyd
34	878	36.2	610	10	ADH61181	Adh61181 Human hyd
35	598.5	24.7	1902	4	ABL13819	Abl13819 Drosophil
36	543	22.4	317	10	ADB90862	Adb90862 Human hyd
37	543	22.4	317	10	ADH61183	Adh61183 Human hyd
38	519	21.4	300	3	AAA00750	Aaa00750 Human col
39	514.5	21.2	3264	4	ABL06061	Abl06061 Drosophil
40	486.5	20.0	1879	6	ABL59530	Abl59530 Human sph
41	486.5	20.0	2344	2	AAQ33394	Aaq33394 R496L ASM
42	486.5	20.0	2344	2	AAT95066	Aat95066 cDNA enco
43	486.5	20.0	2344	9	ACD28698	Acd28698 cDNA enco
44	486.5	20.0	2347	2	AAQ33390	Aaq33390 ASM cDNA,
45	486.5	20.0	2347	2	AAT95067	Aat95067 cDNA enco

ALIGNMENTS

RESULT 1
AAD21343
ID AAD21343 standard; cDNA; 1362 BP.
XX
AC AAD21343;
XX
DT 28-JAN-2002 (first entry)
XX
DE Human nuclear factor kappaB-inducing factor (NFIF)-14b cDNA.
XX
KW Human; NFkappaB; nuclear factor kappaB inducing factor; NFIF-14b;
KW NFIF-7a; immune response; inflammatory response; atherosclerosis;
KW rheumatoid arthritis; NSAID-induced gastropathy; scrapie; sepsis;
KW neurodegenerative disease; autoimmune disease; antisense therapy;
KW renal disease; restenosis; brain injury; viral disease; apoptosis;
KW Alzheimer's disease; pleiotropic cytokine; gene therapy; asthma;
KW Crohn's disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .1362
FT /*tag= a
FT /product= "Human NFIF-14b protein"
XX
PN WO200174900-A2.
XX
PD 11-OCT-2001.
XX

PF 02-APR-2001; 2001WO-US010719.
XX
PR 31-MAR-2000; 2000US-0193905P.
PR 26-JUL-2000; 2000GB-00018307.
XX
PA (AVET) AVENTIS PHARM PROD INC.
XX
PI Kaplow J, Haws T, Rosier M, Denefle P;
XX
DR WPI; 2001-662967/76.
DR P-PSDB; AAE13018.
XX
PT Novel isolated nuclear factor kappaB-inducing factor polypeptides (NFIF-
PT 7a, NFIF-14b), useful for increasing NFkappaB induction in patient, and
PT for manufacturing medicaments for treating or preventing atherosclerosis.
XX
PS Claim 1; Fig 3; 87pp; English.
XX
CC The invention relates to nuclear factor kappaB (NFkappaB) inducing factor
CC NFIF-14b, NFIF-7a (splice variant of NFIF14b) polypeptides and
CC polynucleotides. NFIF-14b and NFIF-7a sequences are useful for inducing
CC NFkappaB in vivo for increasing the activity of NFkappaB- regulated
CC pathways including immune responses. Compositions comprising NFIF
CC sequences are useful for treating or preventing NFkappaB-regulated
CC inflammatory response such as rheumatoid arthritis, atherosclerosis,
CC autoimmune diseases, viral diseases, NSAID-induced gastropathy,
CC neurodegenerative diseases, scrapie, sepsis, apoptosis, Crohn's disease,
CC renal disease, restenosis, brain injury/inflammation, Alzheimer's
CC disease, asthma and improperly regulated expression of pleiotropic
CC cytokines. They are also useful for inhibiting or lowering the expression
CC of NFIF genes or polypeptides, respectively and thus for inhibiting
CC induction of NFkappaB and consequently inhibiting or preventing NFkappaB-
CC regulated immune responses that result in atherosclerosis and other
CC diseases. Polynucleotides of the invention are useful in gene therapy and
CC antisense therapy. The present sequence is human NFIF-14b cDNA
XX
SQ Sequence 1362 BP; 419 A; 291 C; 274 G; 378 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.66e-224	Length:	1362
Score:	2427.00	Matches:	453
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-823-119B-1 (1-453) x AAD21343 (1-1362)

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Qy          1 MetAlaLeuValArgAlaLeuValCysCysLeuLeuThrAlaTrpHisCysArgSerGly 20
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Db          1 ATGGCGCTGGTGCGCGCACTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCCGCTCCGGC 60

Qy         21 LeuGlyLeuProValAlaProAlaGlyGlyArgAsnProProProAlaIleGlyGlnPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTTT 120

Qy         41 TrpHisValThrAspLeuHisLeuAspProThrTyrHisIleThrAspAspHisThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAAA 180

Qy         61 ValCysAlaSerSerLysGlyAlaAsnAlaSerAsnProGlyProPheGlyAspValLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGAGATGTTCTG 240

Qy         81 CysAspSerProTyrGlnLeuIleLeuSerAlaPheAspPheIleLysAsnSerGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATTCTGGACAA 300

Qy        101 GluAlaSerPheMetIleTrpThrGlyAspSerProProHisValProValProGluLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTACCTGAACTC 360

Qy        121 SerThrAspThrValIleAsnValIleThrAsnMetThrThrThrIleGlnSerLeuPhe 140
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Db        361 TCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTTT 420

Qy        141 ProAsnLeuGlnValPheProAlaLeuGlyAsnHisAspTyrTrpProGlnAspGlnLeu 160
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Db        421 CCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGGATCAACTG 480

Qy        161 SerValValThrSerLysValTyrAsnAlaValAlaAsnLeuTrpLysProTrpLeuAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCATGGCTAGAT 540

Qy        181 GluGluAlaIleSerThrLeuArgLysGlyGlyPheTyrSerGlnLysValThrThrAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTACAACTAAT 600

Qy        201 ProAsnLeuArgIleIleSerLeuAsnThrAsnLeuTyrTyrGlyProAsnIleMetThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAATATAATGACA 660

Qy        221 LeuAsnLysThrAspProAlaAsnGlnPheGluTrpLeuGluSerThrLeuAsnAsnSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGAACAACTCT 720

Qy        241 GlnGlnAsnLysGluLysValTyrIleIleAlaHisValProValGlyTyrLeuProSer 260
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Db        721 CAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATCT 780

Qy        261 SerGlnAsnIleThrAlaMetArgGluTyrTyrAsnGluLysLeuIleAspIlePheGln 280
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Db        781 TCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCAA 840

Qy        281 LysTyrSerAspValIleAlaGlyGlnPheTyrGlyHisThrHisArgAspSerIleMet 300
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Qy        301 ValLeuSerAspLysLysGlySerProValAsnSerLeuPheValAlaProAlaValThr 320
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Db        901 GTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACA 960

Qy        321 ProValLysSerValLeuGluLysGlnThrAsnAsnProGlyIleArgLeuPheGlnTyr 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTAT 1020

Qy        341 AspProArgAspTyrLysLeuLeuAspMetLeuGlnTyrTyrLeuAsnLeuThrGluAla 360
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Db       1021 GATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGCG 1080

Qy        361 AsnLeuLysGlyGluSerIleTrpLysLeuGluTyrIleLeuThrGlnThrTyrAspIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACATT 1140

Qy        381 GluAspLeuGlnProGluSerLeuTyrGlyLeuAlaLysGlnPheThrIleLeuAspSer 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAGT 1200

Qy        401 LysGlnPheIleLysTyrTyrAsnTyrPhePheValSerTyrAspSerSerValThrCys 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATGT 1260

Qy        421 AspLysThrCysLysAlaPheGlnIleCysAlaIleMetAsnLeuAspAsnIleSerTyr 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTAT 1320

Qy        441 AlaAspCysLeuLysGlnLeuTyrIleLysHisAsnTyr 453
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Db       1321 GCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTAC 1359
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RESULT 2
ADH61155
ID ADH61155 standard; cDNA; 1763 BP.
XX
AC ADH61155;
XX

DT 25-MAR-2004 (first entry)
XX
DE Human hydrolase-like molecule (HHLM) 5 cDNA #1.
XX
KW Human; hydrolase-like molecule; HHLM; cancer; arteriosclerosis;
KW cytostatic; therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 68. .1429
FT /*tag= a
FT /product= "Human hydrolase-like molecule (HHLM) protein"
XX
PN US2003148363-A1.
XX
PD 07-AUG-2003.
XX
PF 05-FEB-2003; 2003US-00359499.
XX
PR 06-FEB-1998; 98US-00013881.
PR 07-JUL-2000; 2000US-00612473.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Bandman O, Lal P, Hillman JL, Corley NC, Guegler KJ, Shah P;
XX
DR WPI; 2003-897560/82.
DR P-PSDB; ADH61147.
XX
PT New human hydrolase-like molecules (HHLM), useful for preparing a
PT composition for diagnosing, treating or preventing a disease or condition
PT associated with expression of HHLM e.g. cancer or arteriosclerosis.
XX
PS Claim 5; SEQ ID NO 13; 60pp; English.
XX
CC The invention relates to human hydrolase-like molecules (HHLM) and their
CC corresponding nucleic acid sequences. The sequences of the invention are
CC useful for preparing a composition for diagnosing or treating a disease
CC or condition associated with decreased expression or over expression of
CC HHLM e.g., cancer or arteriosclerosis. The present sequence is human
CC hydrolase-like molecule (HHLM) cDNA.
XX
SQ Sequence 1763 BP; 537 A; 356 C; 343 G; 527 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.17e-223	Length:	1763
Score:	2422.00	Matches:	452
Percent Similarity:	99.78%	Conservative:	0
Best Local Similarity:	99.78%	Mismatches:	1
Query Match:	99.79%	Indels:	0
DB:	10	Gaps:	0

US-09-823-119B-1 (1-453) x ADH61155 (1-1763)

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Qy         21 LeuGlyLeuProValAlaProAlaGlyGlyArgAsnProProProAlaIleGlyGlnPhe 40
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Db        128 CTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTTT 187

Qy         41 TrpHisValThrAspLeuHisLeuAspProThrTyrHisIleThrAspAspHisThrLys 60
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Db        188 TGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAAA 247

Qy         61 ValCysAlaSerSerLysGlyAlaAsnAlaSerAsnProGlyProPheGlyAspValLeu 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGAGATGTTCTG 307

Qy         81 CysAspSerProTyrGlnLeuIleLeuSerAlaPheAspPheIleLysAsnSerGlyGln 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 TGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATTCTGGACAA 367

Qy        101 GluAlaSerPheMetIleTrpThrGlyAspSerProProHisValProValProGluLeu 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 GAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTACCTGAACTC 427

Qy        121 SerThrAspThrValIleAsnValIleThrAsnMetThrThrThrIleGlnSerLeuPhe 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 TCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTTT 487

Qy        141 ProAsnLeuGlnValPheProAlaLeuGlyAsnHisAspTyrTrpProGlnAspGlnLeu 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 CCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGGATCAACTG 547

Qy        161 SerValValThrSerLysValTyrAsnAlaValAlaAsnLeuTrpLysProTrpLeuAsp 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 CCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCATGGCTAGAT 607

Qy        181 GluGluAlaIleSerThrLeuArgLysGlyGlyPheTyrSerGlnLysValThrThrAsn 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 GAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTACAACTAAT 667

Qy        201 ProAsnLeuArgIleIleSerLeuAsnThrAsnLeuTyrTyrGlyProAsnIleMetThr 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAATATAATGACA 727

Qy        221 LeuAsnLysThrAspProAlaAsnGlnPheGluTrpLeuGluSerThrLeuAsnAsnSer 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 CTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGAACAACTCT 787

Qy        241 GlnGlnAsnLysGluLysValTyrIleIleAlaHisValProValGlyTyrLeuProSer 260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATCT 847

Qy        261 SerGlnAsnIleThrAlaMetArgGluTyrTyrAsnGluLysLeuIleAspIlePheGln 280
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 TCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCAA 907

Qy        281 LysTyrSerAspValIleAlaGlyGlnPheTyrGlyHisThrHisArgAspSerIleMet 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 AAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTATG 967

Qy        301 ValLeuSerAspLysLysGlySerProValAsnSerLeuPheValAlaProAlaValThr 320
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 GTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACA 1027

Qy        321 ProValLysSerValLeuGluLysGlnThrAsnAsnProGlyIleArgLeuPheGlnTyr 340
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 CCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTAT 1087

Qy        341 AspProArgAspTyrLysLeuLeuAspMetLeuGlnTyrTyrLeuAsnLeuThrGluAla 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1088 GATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGCG 1147

Qy        361 AsnLeuLysGlyGluSerIleTrpLysLeuGluTyrIleLeuThrGlnThrTyrAspIle 380
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1148 AATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACATT 1207

Qy        381 GluAspLeuGlnProGluSerLeuTyrGlyLeuAlaLysGlnPheThrIleLeuAspSer 400
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1208 GAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAGT 1267

Qy        401 LysGlnPheIleLysTyrTyrAsnTyrPhePheValSerTyrAspSerSerValThrCys 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1268 AAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATGT 1327

Qy        421 AspLysThrCysLysAlaPheGlnIleCysAlaIleMetAsnLeuAspAsnIleSerTyr 440
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1328 GATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTAT 1387

Qy        441 AlaAspCysLeuLysGlnLeuTyrIleLysHisAsnTyr 453
              |||||||||||||||||||||||||||||||||||||||
Db       1388 GCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTAC 1426
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RESULT 3
AAC60227
ID   AAC60227 standard; cDNA; 1764 BP.
XX
AC   AAC60227;
XX
DT   13-FEB-2001  (first entry)
XX
DE   Human hydrolase-like molcule 5 cDNA.
XX
KW   Hydrolase-like molecule; human; cell proliferation disorder; autoimmune;
KW   cancer; AIDS; acquired immune deficiency syndrome; ss.
XX
OS   Homo sapiens.
XX
PN   US6132964-A.
XX
PD   17-OCT-2000.
XX
PF   06-FEB-1998;   98US-00013881.
XX
PR   06-FEB-1998;   98US-00013881.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Bandman O,  Hillman JL,  Guegler KJ,  Shah P,  Lal P,  Corley NC;
XX
DR   WPI; 2001-006133/01.
DR   P-PSDB; AAB28794.
XX
PT   New human hydrolase-like molecules (HHLMs) and polynucleotides encoding
PT   the HHLMs, useful for diagnosing, treating or preventing cell
PT   proliferation (e.g. bone cancer) or autoimmune disorders(e.g. AIDS or
PT   asthma).
XX
PS   Claim 5; Col 63-66; 38pp; English.
XX
CC   The present invention relates to isolated and purified cDNA encoding a
CC   human hydrolase-like molecule (HHLM), designated HHLM-1 to HHLM-8. The
CC   HHLM DNAs and polypeptides are useful for diagnosing, treating or
CC   preventing cell proliferation disorders and autoimmune disorders. Cell
CC   proliferation disorders include cancers, autoimmune disorders include
CC   AIDS (acquired immune deficiency syndrome). The present sequence is a
CC   cDNA encoding a HHLM protein of the invention
XX
SQ   Sequence 1764 BP; 537 A; 356 C; 344 G; 527 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.17e-223      Length:          1764
Score:                    2422.00        Matches:         452
Percent Similarity:       99.78%         Conservative:    0
Best Local Similarity:    99.78%         Mismatches:      1
Query Match:              99.79%         Indels:          0
DB:                       4              Gaps:            0

US-09-823-119B-1 (1-453) x AAC60227 (1-1764)

Qy          1 MetAlaLeuValArgAlaLeuValCysCysLeuLeuThrAlaTrpHisCysArgSerGly 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 ATGGCGCTGGTGCGCGCACTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCCGCTCCGGC 128

Qy         21 LeuGlyLeuProValAlaProAlaGlyGlyArgAsnProProProAlaIleGlyGlnPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 CTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTTT 188

Qy         41 TrpHisValThrAspLeuHisLeuAspProThrTyrHisIleThrAspAspHisThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 TGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAAA 248

Qy         61 ValCysAlaSerSerLysGlyAlaAsnAlaSerAsnProGlyProPheGlyAspValLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 GTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGAGATGTTCTG 308

Qy         81 CysAspSerProTyrGlnLeuIleLeuSerAlaPheAspPheIleLysAsnSerGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 TGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATTCTGGACAA 368

Qy        101 GluAlaSerPheMetIleTrpThrGlyAspSerProProHisValProValProGluLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTACCTGAACTC 428

Qy        121 SerThrAspThrValIleAsnValIleThrAsnMetThrThrThrIleGlnSerLeuPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 TCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTTT 488

Qy        141 ProAsnLeuGlnValProProAlaLeuGlyAsnHisAspTyrTrpProGlnAspGlnLeu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGGATCAACTG 548

Qy        161 SerValValThrSerLysValTyrAsnAlaValAlaAsnLeuTrpLysProTrpLeuAsp 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCATGGCTAGAT 608

Qy        181 GluGluAlaIleSerThrLeuArgLysGlyGlyPheTyrSerGlnLysValThrThrAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTACAACTAAT 668

Qy        201 ProAsnLeuArgIleIleSerLeuAsnThrAsnLeuTyrTyrGlyProAsnIleMetThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAATATAATGACA 728

Qy        221 LeuAsnLysThrAspProAlaAsnGlnPheGluTrpLeuGluSerThrLeuAsnAsnSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 CTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGAACAACTCT 788

Qy        241 GlnGlnAsnLysGluLysValTyrIleIleAlaHisValProValGlyTyrLeuProSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 CAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATCT 848

Qy        261 SerGlnAsnIleThrAlaMetArgGluTyrTyrAsnGluLysLeuIleAspIlePheGln 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 TCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCAA 908

Qy        281 LysTyrSerAspValIleAlaGlyGlnPheTyrGlyHisThrHisArgAspSerIleMet 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        909 AAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTATG 968

Qy        301 ValLeuSerAspLysLysGlySerProValAsnSerLeuPheValAlaProAlaValThr 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 GTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACA 1028

Qy        321 ProValLysSerValLeuGluLysGlnThrAsnAsnProGlyIleArgLeuPheGlnTyr 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1029 CCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTAT 1088

Qy        341 AspProArgAspTyrLysLeuLeuAspMetLeuGlnTyrTyrLeuAsnLeuThrGluAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1089 GATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGCG 1148

Qy        361 AsnLeuLysGlyGluSerIleTrpLysLeuGluTyrIleLeuThrGlnThrTyrAspIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1149 AATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACATT 1208

Qy        381 GluAspLeuGlnProGluSerLeuTyrGlyLeuAlaLysGlnPheThrIleLeuAspSer 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1209 GAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAGT 1268

Qy        401 LysGlnPheIleLysTyrTyrAsnTyrPhePheValSerTyrAspSerSerValThrCys 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1269 AAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATGT 1328

Qy        421 AspLysThrCysLysAlaPheGlnIleCysAlaIleMetAsnLeuAspAsnIleSerTyr 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1329 GATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTAT 1388
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Qy        441 AlaAspCysLeuLysGlnLeuTyrIleLysHisAsnTyr 453
              ||||||||||||||||||||||||||||||||||||||||
Db       1389 GCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTAC 1427

RESULT 4
ADA10929
ID   ADA10929 standard; cDNA; 1764 BP.
XX
AC   ADA10929;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human cDNA differentially expressed in colon cancer #33.
XX
KW   ss; differential expression; colon cancer; cancer; human; gene.
XX
OS   Homo sapiens.
XX
PN   US2002160382-A1.
XX
PD   31-OCT-2002.
XX
PF   11-OCT-2001; 2001US-00981353.
XX
PR   11-OCT-2000; 2000US-0239841P.
XX
PA   (LASE/) LASEK A W.
PA   (JONE/) JONES D A.
XX
PI   Lasek AW,  Jones DA;
XX
DR   WPI; 2003-265756/26.
DR   P-PSDB; ADA10930.
XX
PT   New combination comprising cDNAs that are differentially expressed in
PT   colon disorder, useful for diagnosing, treating, staging or monitoring
PT   treatment for colon cancers.
XX
PS   Claim 1; SEQ ID NO 47; 231pp; English.
XX
CC   The invention relates to a combination comprising cDNAs that are
CC   differentially expressed in colon disorder. The methods and compositions
CC   of the present invention are useful for diagnosing, treating, staging or
CC   monitoring treatment for colon cancer. They are also useful in high
CC   throughput methods for using cDNAs to detect differential expression of
CC   nucleic acids in a sample, screening molecules or compounds to identify a
CC   ligand which specifically binds a cDNA and using a protein to screen
CC   molecules or compounds to identify at least one ligand which specifically
CC   binds the protein. The present sequence represents a human cDNA
CC   differentially expressed in colon cancer.
XX
SQ   Sequence 1764 BP; 537 A; 356 C; 344 G; 527 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.17e-223      Length:          1764
Score:                    2422.00        Matches:         452
Percent Similarity:       99.78%         Conservative:    0
Best Local Similarity:    99.78%         Mismatches:      1
Query Match:              99.79%         Indels:          0
DB:                       9              Gaps:            0

US-09-823-119B-1 (1-453) x ADA10929 (1-1764)

Qy          1 MetAlaLeuValArgAlaLeuValCysCysLeuLeuThrAlaTrpHisCysArgSerGly 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 ATGGCGCTGGTGCGCGCACTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCCGCTCCGGC 128

Qy         21 LeuGlyLeuProValAlaProAlaGlyGlyArgAsnProProProAlaIleGlyGlnPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 CTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTTT 188

Qy         41 TrpHisValThrAspLeuHisLeuAspProThrTyrHisIleThrAspAspHisThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 TGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAAA 248

Qy         61 ValCysAlaSerSerLysGlyAlaAsnAlaSerAsnProGlyProPheGlyAspValLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 GTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGAGATGTTCTG 308

Qy         81 CysAspSerProTyrGlnLeuIleLeuSerAlaPheAspPheIleLysAsnSerGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 TGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATTCTGGACAA 368

Qy        101 GluAlaSerPheMetIleTrpThrGlyAspSerProProHisValProValProGluLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTACCTGAACTC 428

Qy        121 SerThrAspThrValIleAsnValIleThrAsnMetThrThrThrIleGlnSerLeuPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 TCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTTT 488

Qy        141 ProAsnLeuGlnValProProAlaLeuGlyAsnHisAspTyrTrpProGlnAspGlnLeu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGGATCAACTG 548

Qy        161 SerValValThrSerLysValTyrAsnAlaValAlaAsnLeuTrpLysProTrpLeuAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCATGGCTAGAT 608

Qy        181 GluGluAlaIleSerThrLeuArgLysGlyGlyPheTyrSerGlnLysValThrThrAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTACAACTAAT 668

Qy        201 ProAsnLeuArgIleIleSerLeuAsnThrAsnLeuTyrTyrGlyProAsnIleMetThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAATATAATGACA 728

Qy        221 LeuAsnLysThrAspProAlaAsnGlnPheGluTrpLeuGluSerThrLeuAsnAsnSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 CTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGAACAACTCT 788

Qy        241 GlnGlnAsnLysGluLysValTyrIleIleAlaHisValProValGlyTyrLeuProSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 CAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATCT 848

Qy        261 SerGlnAsnIleThrAlaMetArgGluTyrTyrAsnGluLysLeuIleAspIlePheGln 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 TCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCAA 908

Qy        281 LysTyrSerAspValIleAlaGlyGlnPheTyrGlyHisThrHisArgAspSerIleMet 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        909 AAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTATG 968

Qy        301 ValLeuSerAspLysLysGlySerProValAsnSerLeuPheValAlaProAlaValThr 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 GTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACA 1028

Qy        321 ProValLysSerValLeuGluLysGlnThrAsnAsnProGlyIleArgLeuPheGlnTyr 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1029 CCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTAT 1088

Qy        341 AspProArgAspTyrLysLeuLeuAspMetLeuGlnTyrTyrLeuAsnLeuThrGluAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1089 GATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGCG 1148

Qy        361 AsnLeuLysGlyGluSerIleTrpLysLeuGluTyrIleLeuThrGlnThrTyrAspIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1149 AATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACATT 1208

Qy        381 GluAspLeuGlnProGluSerLeuTyrGlyLeuAlaLysGlnPheThrIleLeuAspSer 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1209 GAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAGT 1268

Qy        401 LysGlnPheIleLysTyrTyrAsnTyrPhePheValSerTyrAspSerSerValThrCys 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1269 AAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATGT 1328
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Qy        421 AspLysThrCysLysAlaPheGlnIleCysAlaIleMetAsnLeuAspAsnIleSerTyr 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1329 GATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTAT 1388

Qy        441 AlaAspCysLeuLysGlnLeuTyrIleLysHisAsnTyr 453
              |||||||||||||||||||||||||||||||||||||
Db       1389 GCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTAC 1427
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RESULT 5
ADB90834
ID ADB90834 standard; cDNA; 1764 BP.
XX
AC ADB90834;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human cDNA encoding hydrolase-like molecule, HHLM 5, INCYTE 1376382.
XX
KW Human; hydrolase-like molecule; HHLM; cell proliferation disorder;
KW arteriosclerosis; atherosclerosis; bursitis; psoriasis; cancer;
KW autoimmune disorder; AIDS; Addison's disease;
KW adult respiratory distress syndrome; anaemia; asthma; diabetes mellitus;
KW ss; gene.
XX
OS Homo sapiens.
XX
PN US6518029-B1.
XX
PD 11-FEB-2003.
XX
PF 07-JUL-2000; 2000US-00612473.
XX
PR 06-FEB-1998; 98US-00013881.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Bandman O, Lal P, Hillman JL, Corley NC, Guegler KJ, Shah P;
XX
DR WPI; 2003-742789/70.
DR P-PSDB; ADB90826.
XX
PT New human hydrolase-like molecules, useful for treating or preventing
PT cell proliferation disorders (e.g. atherosclerosis or cancers) and
PT autoimmune disorders (e.g. AIDS, Addison's disease, anemia, asthma and
PT diabetes mellitus).
XX
PS Example 6; Col 65-68; 55pp; English.
XX
CC The invention relates to a new isolated polypeptide comprising a human
CC hydrolase-like molecule, termed HHLM1-8 appearing as ADB90822 - ADB90829,
CC a naturally occurring polypeptide comprising a sequence which is at least
CC 81% identical the HHLM, a biologically active fragment of an HHLM or an
CC immunogenic fragment comprising at least 15 contiguous amino acids. Also
CC included are a composition comprising an HHLM and an excipient, a method
CC for screening a compound as an agonist or antagonist of HHLM (by exposing
CC a sample comprising HHLM to a compound, and detecting agonist or
CC antagonist activity in the sample), a method for screening a compound
CC that specifically binds to HHLM (by combining HHLM with at least one test
CC compound, and detecting binding of HHLM to the test compound) and a
CC method for screening a compound that modulates the activity of HHLM. The
CC human hydrolase-like molecules (HHLM), agonists and antagonists useful
CC for treating or preventing cell proliferation disorders (e.g.
CC arteriosclerosis, atherosclerosis, bursitis, psoriasis, and cancers) and
CC autoimmune disorders (e.g. AIDS, Addison's disease, adult respiratory
CC distress syndrome, anaemia, asthma and diabetes mellitus). The HHLM
CC polypeptides are useful in preparing antibodies that specifically bind to
CC the polypeptides. Nucleic acids encoding HHLM are useful in generating
CC probes for mapping naturally occurring genomic sequences, in detecting
CC differences in the chromosomal location due to translocation or
CC inversion, and in screening libraries of compounds in drug screening
CC techniques. The present sequence encodes an HHLM of the invention.
XX

SQ Sequence 1764 BP; 537 A; 356 C; 344 G; 527 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.17e-223	Length:	1764
Score:	2422.00	Matches:	452
Percent Similarity:	99.78%	Conservative:	0
Best Local Similarity:	99.78%	Mismatches:	1
Query Match:	99.79%	Indels:	0
DB:	10	Gaps:	0

US-09-823-119B-1 (1-453) x ADB90834 (1-1764)

```
Qy          1 MetAlaLeuValArgAlaLeuValCysCysLeuLeuThrAlaTrpHisCysArgSerGly 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 ATGGCGCTGGTGCGCGCACTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCCGCTCCGGC 128

Qy         21 LeuGlyLeuProValAlaProAlaGlyGlyArgAsnProProProAlaIleGlyGlnPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 CTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTTT 188

Qy         41 TrpHisValThrAspLeuHisLeuAspProThrTyrHisIleThrAspAspHisThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 TGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAAA 248

Qy         61 ValCysAlaSerSerLysGlyAlaAsnAlaSerAsnProGlyProPheGlyAspValLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 GTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGAGATGTTCTG 308

Qy         81 CysAspSerProTyrGlnLeuIleLeuSerAlaPheAspPheIleLysAsnSerGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 TGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATTCTGGACAA 368

Qy        101 GluAlaSerPheMetIleTrpThrGlyAspSerProProHisValProValProGluLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTACCTGAACTC 428

Qy        121 SerThrAspThrValIleAsnValIleThrAsnMetThrThrThrIleGlnSerLeuPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 TCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTTT 488

Qy        141 ProAsnLeuGlnValProProAlaLeuGlyAsnHisAspTyrTrpProGlnAspGlnLeu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGGATCAACTG 548

Qy        161 SerValValThrSerLysValTyrAsnAlaValAlaAsnLeuTrpLysProTrpLeuAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCATGGCTAGAT 608

Qy        181 GluGluAlaIleSerThrLeuArgLysGlyGlyPheTyrSerGlnLysValThrThrAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTACAACTAAT 668

Qy        201 ProAsnLeuArgIleIleSerLeuAsnThrAsnLeuTyrTyrGlyProAsnIleMetThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAATATAATGACA 728

Qy        221 LeuAsnLysThrAspProAlaAsnGlnPheGluTrpLeuGluSerThrLeuAsnAsnSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 CTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGAACAACTCT 788

Qy        241 GlnGlnAsnLysGluLysValTyrIleIleAlaHisValProValGlyTyrLeuProSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 CAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATCT 848

Qy        261 SerGlnAsnIleThrAlaMetArgGluTyrTyrAsnGluLysLeuIleAspIlePheGln 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 TCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCAA 908

Qy        281 LysTyrSerAspValIleAlaGlyGlnPheTyrGlyHisThrHisArgAspSerIleMet 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        909 AAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTATG 968

Qy        301 ValLeuSerAspLysLysGlySerProValAsnSerLeuPheValAlaProAlaValThr 320
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                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 GTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACA 1028

Qy        321 ProValLysSerValLeuGluLysGlnThrAsnAsnProGlyIleArgLeuPheGlnTyr 340
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1029 CCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTAT 1088

Qy        341 AspProArgAspTyrLysLeuLeuAspMetLeuGlnTyrTyrLeuAsnLeuThrGluAla 360
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1089 GATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGCG 1148

Qy        361 AsnLeuLysGlyGluSerIleTrpLysLeuGluTyrIleLeuThrGlnThrTyrAspIle 380
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1149 AATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACATT 1208

Qy        381 GluAspLeuGlnProGluSerLeuTyrGlyLeuAlaLysGlnPheThrIleLeuAspSer 400
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1209 GAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAGT 1268

Qy        401 LysGlnPheIleLysTyrTyrAsnTyrPhePheValSerTyrAspSerSerValThrCys 420
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1269 AAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATGT 1328

Qy        421 AspLysThrCysLysAlaPheGlnIleCysAlaIleMetAsnLeuAspAsnIleSerTyr 440
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1329 GATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTAT 1388

Qy        441 AlaAspCysLeuLysGlnLeuTyrIleLysHisAsnTyr 453
                |||||||||||||||||||||||||||||||||||||
Db       1389 GCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTAC 1427

RESULT 6
ADJ45508
ID   ADJ45508 standard; cDNA; 1768 BP.
XX
AC   ADJ45508;
XX
DT   06-MAY-2004  (first entry)
XX
DE   cDNA encoding LXR-ligand induced transcript seq id 39.
XX
KW   LXR; liver X receptor; cholesterol; gallstone; atherosclerosis;
KW   lipid storage disease; obesity; diabetes; hypercholesterolaemia;
KW   LXR-ligand induced 1; LXRLI1; human; LXR-ligand induced transcript;
KW   LXR regulated gene; ss; gene.
XX
OS   Homo sapiens.
XX
PN   US2004023276-A1.
XX
PD   05-FEB-2004.
XX
PF   02-MAY-2003; 2003US-00429160.
XX
PR   03-MAY-2002; 2002US-0377714P.
XX
PA   (WARD/) WARD T R.
PA   (MAOM/) MAO M.
PA   (LINS/) LINSLEY P S.
PA   (LUND/) LUND E.
XX
PI   Ward TR,  Mao M,  Linsley PS,  Lund E;
XX
DR   WPI; 2004-224687/21.
DR   P-PSDB; ADJ45509.
XX
PT   New purified Liver X receptor (LXR) nucleic acids, useful for diagnosing
PT   a disease involving LXR activity, such as cholesterol gallstones,
PT   atherosclerosis, lipid storage diseases, obesity, diabetes, or
PT   hypercholesterolemia.
XX
PS   Example 1; SEQ ID NO 39; 141pp; English.
XX
CC   The invention describes a purified nucleic acid comprising a fully
CC   defined sequence of 1586 bp (SEQ ID NO: 1) as given in the specification,
CC   or its complement. The methods and compositions are useful for diagnosing
CC   a disease or disorder involving LXR (liver X receptor) activity in a
CC   sample by detecting an increase or decrease in the transcript level
CC   relative to the amount present in an analogous sample from a subject not
CC   having the disease or disorder or not subjected to therapy, wherein the
CC   disease or disorder is cholesterol gallstones, atherosclerosis, lipid
CC   storage diseases, obesity, diabetes, or hypercholesterolaemia. They are
CC   also used to identify a compound that changes LXR activity, wherein the
CC   compound changes the estimated level of LXR activity in a sample from the
CC   subject contacted with the compound relative to the estimated level of
CC   LXR activity in an analogous sample from the subject not contacted with
CC   the compound. This sequence encodes an LXR regulated protein.
XX
SQ   Sequence 1768 BP; 540 A; 358 C; 346 G; 524 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.17e-223       Length:          1768
Score:                    2422.00         Matches:         452
Percent Similarity:       99.78%          Conservative:    0
Best Local Similarity:    99.78%          Mismatches:      1
Query Match:              99.79%          Indels:          0
DB:                       12              Gaps:            0

US-09-823-119B-1 (1-453) x ADJ45508 (1-1768)

Qy          1 MetAlaLeuValArgAlaLeuValCysCysLeuLeuThrAlaTrpHisCysArgSerGly 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 ATGGCGCTGGTGCGCGCACTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCCGCTCCGGC 137

Qy         21 LeuGlyLeuProValAlaProAlaGlyGlyArgAsnProProProAlaIleGlyGlnPhe 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 CTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTTT 197

Qy         41 TrpHisValThrAspLeuHisLeuAspProThrTyrHisIleThrAspAspHisThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAAA 257

Qy         61 ValCysAlaSerSerLysGlyAlaAsnAlaSerAsnProGlyProPheGlyAspValLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 GTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGAGATGTTCTG 317

Qy         81 CysAspSerProTyrGlnLeuIleLeuSerAlaPheAspPheIleLysAsnSerGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 TGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATTCTGGACAA 377

Qy        101 GluAlaSerPheMetIleTrpThrGlyAspSerProProHisValProValProGluLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTACCTGAACTC 437

Qy        121 SerThrAspThrValIleAsnValIleThrAsnMetThrThrThrIleGlnSerLeuPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 TCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTTT 497

Qy        141 ProAsnLeuGlnValPheProAlaLeuGlyAsnHisAspTyrTrpProGlnAspGlnLeu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 CCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGGATCAACTG 557

Qy        161 SerValValThrSerLysValTyrAsnAlaValAlaAsnLeuTrpLysProTrpLeuAsp 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 CCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCATGGCTAGAT 617

Qy        181 GluGluAlaIleSerThrLeuArgLysGlyGlyPheTyrSerGlnLysValThrThrAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 GAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTACAACTAAT 677

Qy        201 ProAsnLeuArgIleIleSerLeuAsnThrAsnLeuTyrTyrGlyProAsnIleMetThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 CCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAATATAATGACA 737

Qy        221 LeuAsnLysThrAspProAlaAsnGlnPheGluTrpLeuGluSerThrLeuAsnAsnSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        738 CTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGAACAACTCT 797

Qy        241 GlnGlnAsnLysGluLysValTyrIleIleAlaHisValProValGlyTyrLeuProSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        798 CAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATCT 857

Qy        261 SerGlnAsnIleThrAlaMetArgGluTyrTyrAsnGluLysLeuIleAspIlePheGln 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        858 TCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCAA 917

Qy        281 LysTyrSerAspValIleAlaGlyGlnPheTyrGlyHisThrHisArgAspSerIleMet 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        918 AAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTATG 977

Qy        301 ValLeuSerAspLysLysGlySerProValAsnSerLeuPheValAlaProAlaValThr 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        978 GTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACA 1037

Qy        321 ProValLysSerValLeuGluLysGlnThrAsnAsnProGlyIleArgLeuPheGlnTyr 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1038 CCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTAT 1097

Qy        341 AspProArgAspTyrLysLeuLeuAspMetLeuGlnTyrTyrLeuAsnLeuThrGluAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1098 GATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGCG 1157

Qy        361 AsnLeuLysGlyGluSerIleTrpLysLeuGluTyrIleLeuThrGlnThrTyrAspIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1158 AATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACATT 1217

Qy        381 GluAspLeuGlnProGluSerLeuTyrGlyLeuAlaLysGlnPheThrIleLeuAspSer 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1218 GAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAGT 1277

Qy        401 LysGlnPheIleLysTyrTyrAsnTyrPhePheValSerTyrAspSerSerValThrCys 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1278 AAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATGT 1337

Qy        421 AspLysThrCysLysAlaPheGlnIleCysAlaIleMetAsnLeuAspAsnIleSerTyr 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1338 GATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTAT 1397

Qy        441 AlaAspCysLeuLysGlnLeuTyrIleLysHisAsnTyr 453
              |||||||||||||||||||||||||||||||||||||||
Db       1398 GCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTAC 1436
```

RESULT 7
AAS62765
ID AAS62765 standard; cDNA; 1783 BP.
XX
AC AAS62765;
XX
DT 14-FEB-2002 (first entry)
XX
DE cDNA sequence #552 encoding novel human secreted protein.
XX
KW Human secreted protein; hyperproliferative disorder; autoimmune disorder;
KW immune deficiency disorder; blood disorder; inflammatory disorder;
KW infectious disorder; gene therapy; antimicrobial; hepatotropic;
KW immunosuppressive; antirheumatic; ss.
XX
OS Homo sapiens.
XX
PN WO200177291-A2.
XX
PD 18-OCT-2001.
XX
PF 29-MAR-2001; 2001WO-US010485.
XX
PR 06-APR-2000; 2000US-0195604P.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;
PI Gulukota K, Graham JR;
XX
DR WPI; 2002-010900/01.
XX
PT New polynucleotides encoding secreted proteins useful for treating e.g.
PT asthma, HIV and Crohn's disease.
XX
PS Claim 1; Page 356; 391pp; English.
XX
CC The present invention relates to the isolation of novel cDNA sequences
CC which encode human secreted proteins. The cDNA sequences have been
CC derived from a variety of human tissues. The invention also provides a
CC method for producing proteins from these polynucleotide sequences. The
CC proteins are useful for identifying compounds that modulate their
CC activity and production, and the cell is also useful for identifying
CC compounds that modulate expression of the polynucleotide sequences
CC encoding the secreted proteins. The sequences of the invention are useful
CC for treating diseases such as hyperproliferative disorders (e.g. cancer),
CC immune deficiency disorders (e.g. severe combined immunodeficiency
CC (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders
CC (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis) and
CC infectious disorders (e.g. hepatitis). The polynucleotide sequences of
CC the invention are also useful in gene therapy. AAS62214-AAS62838
CC represent the cDNA sequences of the invention that encode for novel human
CC secreted proteins
XX
SQ Sequence 1783 BP; 523 A; 376 C; 348 G; 536 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.77e-223	Length:	1783
Score:	2413.00	Matches:	451
Percent Similarity:	99.56%	Conservative:	0
Best Local Similarity:	99.56%	Mismatches:	2
Query Match:	99.42%	Indels:	0
DB:	6	Gaps:	0

US-09-823-119B-1 (1-453) x AAS62765 (1-1783)

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Qy          1 MetAlaLeuValArgAlaLeuValCysCysLeuLeuThrAlaTrpHisCysArgSerGly 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 ATGGCGCTGGTGCGCGCACTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCCGCTCCGGC 172

Qy         21 LeuGlyLeuProValAlaProAlaGlyGlyArgAsnProProProAlaIleGlyGlnPhe 40
              |||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db        173 CTCGGGCTGCCCGTGGCGCCCGCATGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTTT 232

Qy         41 TrpHisValThrAspLeuHisLeuAspProThrTyrHisIleThrAspAspHisThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 TGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAAA 292

Qy         61 ValCysAlaSerSerLysGlyAlaAsnAlaSerAsnProGlyProPheGlyAspValLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 GTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGAGATGTTCTG 352

Qy         81 CysAspSerProTyrGlnLeuIleLeuSerAlaPheAspPheIleLysAsnSerGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 TGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATTCTGGACAA 412

Qy        101 GluAlaSerPheMetIleTrpThrGlyAspSerProProHisValProValProGluLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 GAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTACCTGAACTC 472

Qy        121 SerThrAspThrValIleAsnValIleThrAsnMetThrThrThrIleGlnSerLeuPhe 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 TCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTTT 532

Qy        141 ProAsnLeuGlnValPheProAlaLeuGlyAsnHisAspTyrTrpProGlnAspGlnLeu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 CCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGGATCAACTG 592

Qy        161 SerValValThrSerLysValTyrAsnAlaValAlaAsnLeuTrpLysProTrpLeuAsp 180
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        593 CCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCATGGCTAGAT 652

Qy        181 GluGluAlaIleSerThrLeuArgLysGlyGlyPheTyrSerGlnLysValThrThrAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 GAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTACAACTAAT 712

Qy        201 ProAsnLeuArgIleIleSerLeuAsnThrAsnLeuTyrTyrGlyProAsnIleMetThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 CCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAATATAATGACA 772

Qy        221 LeuAsnLysThrAspProAlaAsnGlnPheGluTrpLeuGluSerThrLeuAsnAsnSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 CTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGAACAACTCT 832

Qy        241 GlnGlnAsnLysGluLysValTyrIleIleAlaHisValProValGlyTyrLeuProSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 CAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATCT 892

Qy        261 SerGlnAsnIleThrAlaMetArgGluTyrTyrAsnGluLysLeuIleAspIlePheGln 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 TCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCAA 952

Qy        281 LysTyrSerAspValIleAlaGlyGlnPheTyrGlyHisThrHisArgAspSerIleMet 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        953 AAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTATG 1012

Qy        301 ValLeuSerAspLysLysGlySerProValAsnSerLeuPheValAlaProAlaValThr 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1013 GTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACA 1072

Qy        321 ProValLysSerValLeuGluLysGlnThrAsnAsnProGlyIleArgLeuPheGlnTyr 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1073 CCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTAT 1132

Qy        341 AspProArgAspTyrLysLeuLeuAspMetLeuGlnTyrTyrLeuAsnLeuThrGluAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1133 GATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGCG 1192

Qy        361 AsnLeuLysGlyGluSerIleTrpLysLeuGluTyrIleLeuThrGlnThrTyrAspIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1193 AATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACATT 1252

Qy        381 GluAspLeuGlnProGluSerLeuTyrGlyLeuAlaLysGlnPheThrIleLeuAspSer 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1253 GAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAGT 1312

Qy        401 LysGlnPheIleLysTyrTyrAsnTyrPhePheValSerTyrAspSerSerValThrCys 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1313 AAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATGT 1372

Qy        421 AspLysThrCysLysAlaPheGlnIleCysAlaIleMetAsnLeuAspAsnIleSerTyr 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1373 GATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTAT 1432

Qy        441 AlaAspCysLeuLysGlnLeuTyrIleLysHisAsnTyr 453
              |||||||||||||||||||||||||||||||||||||||
Db       1433 GCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTAC 1471

RESULT 8
AAS94849
ID   AAS94849 standard; DNA; 1746 BP.
XX
AC   AAS94849;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Human DNA sequence #104 expressed during foam cell differentiation.
XX
KW   Human; foam cell differentiation; atherosclerosis; cerebral stroke;
KW   cardiovascular disorder; coronary artery disease; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200177389-A2.
XX
PD   18-OCT-2001.
XX
PF   04-APR-2001; 2001WO-US011128.
XX
PR   05-APR-2000; 2000US-0195106P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Shiffman D,  Somogyi R,  Lawn R,  Seilhamer JJ,  Porter GJ,  Mikita T;
PI   Tai J;
XX
DR   WPI; 2002-010925/01.
XX
PT   Composition useful for diagnosis of conditions, disorders or diseases
PT   associated with atherosclerosis, comprises several polynucleotides that
PT   are differentially expressed in foam cell development.
XX
PS   Claim 1; Page 156; 315pp; English.
XX
CC   The present invention relates to the isolation of human polynucleotide
CC   sequences that are differentially expressed during foam cell
CC   differentiation. The polynucleotide sequences of the invention or a
CC   composition comprising these polynucleotides are useful as a high
CC   throughput method for detecting altered expression of one or more
CC   polynucleotides in a sample. The polynucleotides can be used in the
CC   diagnosis of disorders associated with foam cell development such as
CC   atherosclerosis, cerebral stroke, and cardiovascular disorders such as
CC   coronary artery disease. The polynucleotide sequences can also be used as
CC   PCR primers and probes. The polynucleotides of the invention are also
CC   useful in gene therapy. AAS94746-AAS95021 represent the human
CC   polynucleotide sequences of the invention which are differentially
CC   expressed during foam cell differentiation
XX
SQ   Sequence 1746 BP; 521 A; 356 C; 342 G; 527 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.07e-222       Length:          1746
Score:                  2409.00         Matches:         452
Percent Similarity:     99.56%          Conservative:    0
Best Local Similarity:  99.56%          Mismatches:      1
Query Match:            99.26%          Indels:          1
DB:                     6               Gaps:            0

US-09-823-119B-1 (1-453) x AAS94849 (1-1746)

Qy          1 MetAlaLeuValArgAlaLeu-ValCysCysLeuLeuThrAlaTrpHisCysArgSerGl 20
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         69 ATGGCGCTGGTGCGCGCACTTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCCGCTCCGG 128

Qy         20 yLeuGlyLeuProValAlaProAlaGlyGlyArgAsnProProProAlaIleGlyGlnPh 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 CCTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTT 188

Qy         40 eTrpHisValThrAspLeuHisLeuAspProThrTyrHisIleThrAspAspHisThrLy 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 TTGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAA 248

Qy         60 sValCysAlaSerSerLysGlyAlaAsnAlaSerAsnProGlyProPheGlyAspValLe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AGTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGAGATGTTCT 308

Qy         80 uCysAspSerProTyrGlnLeuIleLeuSerAlaPheAspPheIleLysAsnSerGlyGl 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 GTGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATTCTGGACA 368

Qy        100 nGluAlaSerPheMetIleTrpThrGlyAspSerProProHisValProValProGluLe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 AGAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTACCTGAACT 428

Qy        120 uSerThrAspThrValIleAsnValIleThrAsnMetThrThrThrIleGlnSerLeuPh 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        429 CTCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTT 488

Qy        140 eProAsnLeuGlnValPheProAlaLeuGlyAsnHisAspTyrTrpProGlnAspGlnLe 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 TCCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGGATCAACT 548

Qy        160 uSerValValThrSerLysValTyrAsnAlaValAlaAsnLeuTrpLysProTrpLeuAs 180
              |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 GCCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCATGGCTAGA 608

Qy        180 pGluGluAlaIleSerThrLeuArgLysGlyGlyPheTyrSerGlnLysValThrThrAs 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 TGAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTACAACTAA 668

Qy        200 nProAsnLeuArgIleIleSerLeuAsnThrAsnLeuTyrTyrGlyProAsnIleMetTh 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 TCCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAATATAATGAC 728

Qy        220 rLeuAsnLysThrAspProAlaAsnGlnPheGluTrpLeuGluSerThrLeuAsnAsnSe 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 ACTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGAACAACTC 788

Qy        240 rGlnGlnAsnLysGluLysValTyrIleIleAlaHisValProValGlyTyrLeuProSe 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 TCAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATC 848

Qy        260 rSerGlnAsnIleThrAlaMetArgGluTyrTyrAsnGluLysLeuIleAspIlePheGl 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 TTCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCA 908

Qy        280 nLysTyrSerAspValIleAlaGlyGlnPheTyrGlyHisThrHisArgAspSerIleMe 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        909 AAAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTAT 968

Qy        300 tValLeuSerAspLysLysGlySerProValAsnSerLeuPheValAlaProAlaValTh 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 GGTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTAC 1028

Qy        320 rProValLysSerValLeuGluLysGlnThrAsnAsnProGlyIleArgLeuPheGlnTy 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1029 ACCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTA 1088

Qy        340 rAspProArgAspTyrLysLeuLeuAspMetLeuGlnTyrTyrLeuAsnLeuThrGluAl 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1089 TGATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGC 1148

Qy        360 aAsnLeuLysGlyGluSerIleTrpLysLeuGluTyrIleLeuThrGlnThrTyrAspIl 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1149 GAATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACAT 1208

Qy        380 eGluAspLeuGlnProGluSerLeuTyrGlyLeuAlaLysGlnPheThrIleLeuAspSe 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1209 TGAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAG 1268

Qy        400 rLysGlnPheIleLysTyrTyrAsnTyrPhePheValSerTyrAspSerSerValThrCy 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1269 TAAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATG 1328

Qy        420 sAspLysThrCysLysAlaPheGlnIleCysAlaIleMetAsnLeuAspAsnIleSerTy 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1329 TGATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTA 1388

Qy        440 rAlaAspCysLeuLysGlnLeuTyrIleLysHisAsnTyr 453
              |||||||||||||||||||||||||||||||||||||||
Db       1389 TGCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTAC 1428

RESULT 9
ADF81833
ID   ADF81833 standard; DNA; 2505 BP.
XX
AC   ADF81833;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Leukaemia-related DNA sequence #2389.
XX
KW   Cytostatic; Gene therapy; leukaemia; ss.
XX
OS   Unidentified.
XX
PN   WO2003039443-A2.
XX
PD   15-MAY-2003.
XX
PF   04-NOV-2002; 2002WO-EP012303.
XX
PR   05-NOV-2001; 2001EP-00126244.
PR   30-APR-2002; 2002EP-00009758.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA   (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA   (HAFE/) HAFERLACH T.
PA   (SCHO/) SCHOCH C.
PA   (KERN/) KERN W.
XX
PI   Haferlach T,  Schoch C,  Kern W,  Kohlmann A,  Schnittger S,  Dugas M;
PI   Eils R,  Brors B,  Mergenthaler S;
XX
DR   WPI; 2003-505037/47.
XX
PT   Determining the subtype of leukemia cells and whether a patient sample
PT   contains leukemia cells or other cells, useful for treating leukemia,
PT   comprises determining the expression profile of a group of markers in a
PT   patient sample.
XX
PS   Disclosure; SEQ ID NO 2389; 2938pp; English.
XX
CC   The present invention relates to a method (M1) for determining the
CC   subtype of leukaemia cells and whether a patient sample contains
CC   leukaemia cells. The method comprises determining the expression profile
CC   of a group of markers in a patient sample. The method is useful for
CC   determining the presence of leukaemia cells, its types or subtypes, and
CC   for the preparation of a medicament for treating leukaemia.
XX
SQ   Sequence 2505 BP; 730 A; 537 C; 482 G; 737 T; 0 U; 19 Other;

Alignment Scores:
Pred. No.:                5.7e-217        Length:          2505
Score:                    2355.00         Matches:         445
Percent Similarity:       98.02%          Conservative:    0
Best Local Similarity:    98.02%          Mismatches:      8
Query Match:              97.03%          Indels:          1
DB:                       10              Gaps:            0

US-09-823-119B-1 (1-453) x ADF81833 (1-2505)

Qy          1 MetAlaLeuValArgAlaLeuValCysCys-LeuLeuThrAlaTrpHisCysArgSerGl 20
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db        590 ATGGCGCTGGTGCGCGCACTCGTCTGCTGCCNTGCTGACTGCCTGGCACTGCCGCTCCGG 649

Qy         20 yLeuGlyLeuProValAlaProAlaGlyGlyArgAsnProProProAlaIleGlyGlnPh 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        650 CCTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGNNAGTT 709

Qy         40 eTrpHisValThrAspLeuHisLeuAspProThrTyrHisIleThrAspAspHisThrLy 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 NTNNNATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAA 769

Qy         60 sValCysAlaSerSerLysGlyAlaAsnAlaSerAsnProGlyProPheGlyAspValLe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||
Db        770 AGTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTNTGGAGATGTTCT 829

Qy         80 uCysAspSerProTyrGlnLeuIleLeuSerAlaPheAspPheIleLysAsnSerGlyGl 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        830 GTGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATTCTGGACA 889
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Qy       100 nGluAlaSerPheMetIleTrpThrGlyAspSerProProHisValProValProGluLe 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       890 AGAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTACCTGAACT 949

Qy       120 uSerThrAspThrValIleAsnValIleThrAsnMetThrThrThrIleGlnSerLeuPh 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       950 CTCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTT 1009

Qy       140 eProAsnLeuGlnValPheProAlaLeuGlyAsnHisAspTyrTrpProGlnAspGlnLe 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1010 TCCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGGATCAACT 1069

Qy       160 uSerValValThrSerLysValTyrAsnAlaValAlaAsnLeuTrpLysProTrpLeuAs 180
             |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1070 GCCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCATGGCTAGA 1129

Qy       180 pGluGluAlaIleSerThrLeuArgLysGlyGlyPheTyrSerGlnLysValThrThrAs 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1130 TGAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTACAACTAA 1189

Qy       200 nProAsnLeuArgIleIleSerLeuAsnThrAsnLeuTyrTyrGlyProAsnIleMetTh 220
             ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db      1190 TCCAAACCTTAGGATCATCAGTCTANACACAAACTTGTACTACGGCCCAAATATAATGAC 1249

Qy       220 rLeuAsnLysThrAspProAlaAsnGlnPheGluTrpLeuGluSerThrLeuAsnAsnSe 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1250 ACTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGAACAACTC 1309

Qy       240 rGlnGlnAsnLysGluLysValTyrIleIleAlaHisValProValGlyTyrLeuProSe 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1310 TCAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATC 1369

Qy       260 rSerGlnAsnIleThrAlaMetArgGluTyrTyrAsnGluLysLeuIleAspIlePheGl 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1370 TTCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCA 1429

Qy       280 nLysTyrSerAspValIleAlaGlyGlnPheTyrGlyHisThrHisArgAspSerIleMe 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1430 AAAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTAT 1489

Qy       300 tValLeuSerAspLysLysGlySerProValAsnSerLeuPheValAlaProAlaValTh 320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1490 GGTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTAC 1549

Qy       320 rProValLysSerValLeuGluLysGlnThrAsnAsnProGlyIleArgLeuPheGlnTy 340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1550 ACCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTA 1609

Qy       340 rAspProArgAspTyrLysLeuLeuAspMetLeuGlnTyrTyrLeuAsnLeuThrGluAl 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1610 TGATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGC 1669

Qy       360 aAsnLeuLysGlyGluSerIleTrpLysLeuGluTyrIleLeuThrGlnThrTyrAspIl 380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1670 GAATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACAT 1729

Qy       380 eGluAspLeuGlnProGluSerLeuTyrGlyLeuAlaLysGlnPheThrIleLeuAspSe 400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1730 TGAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAG 1789

Qy       400 rLysGlnPheIleLysTyrTyrAsnTyrPhePheValSerTyrAspSerSerValThrCy 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1790 TAAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATG 1849

Qy       420 sAspLysThrCysLysAlaPheGlnIleCysAlaIleMetAsnLeuAspAsnIleSerTy 440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1850 TGATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTA 1909

Qy       440 rAlaAspCysLeuLysGlnLeuTyrIleLysHisAsnTyr 453
             ||||||||||||||||||||||||||||||||||||||||
Db      1910 TGCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTAC 1949

RESULT 10
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AAI61110
ID   AAI61110 standard; cDNA; 1873 BP.
XX
AC   AAI61110;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 5099.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US034263.
XX
PR   23-DEC-1999;   99US-00471275.
PR   21-JAN-2000; 2000US-00488725.
PR   25-APR-2000; 2000US-00552317.
PR   20-JUN-2000; 2000US-00598042.
PR   19-JUL-2000; 2000US-00620312.
PR   03-AUG-2000; 2000US-00653450.
PR   14-SEP-2000; 2000US-00662191.
PR   19-OCT-2000; 2000US-00693036.
PR   29-NOV-2000; 2000US-00727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J,  Zhao QA;
PI   Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   P-PSDB; AAM41954.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders such
PT   as central nervous system injuries.
XX
PS   Claim 1; SEQ ID NO 5099; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC   encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders. Note: The sequence data for this patent did not form
CC   part of the printed specification
XX
SQ   Sequence 1873 BP; 596 A; 359 C; 335 G; 583 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.12e-204      Length:          1873
Score:                  2223.00        Matches:         416
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            91.59%         Indels:          0
DB:                     4              Gaps:            0
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```
US-09-823-119B-1 (1-453) x AAI61110 (1-1873)

Qy         38 GlyGlnPheTrpHisValThrAspLeuHisLeuAspProThrTyrHisIleThrAspAsp 57
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Db        303 GGACAGTTTTGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGAC 362

Qy         58 HisThrLysValCysAlaSerSerLysGlyAlaAsnAlaSerAsnProGlyProPheGly 77
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Db        363 CACACAAAAGTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGA 422

Qy         78 AspValLeuCysAspSerProTyrGlnLeuIleLeuSerAlaPheAspPheIleLysAsn 97
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Db        423 GATGTTCTGTGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAAT 482

Qy         98 SerGlyGlnGluAlaSerPheMetIleTrpThrGlyAspSerProProHisValProVal 117
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Db        483 TCTGGACAAGAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTA 542

Qy        118 ProGluLeuSerThrAspThrValIleAsnValIleThrAsnMetThrThrThrIleGln 137
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Db        543 CCTGAACTCTCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAG 602

Qy        138 SerLeuProProAsnLeuGlnValProProAlaLeuGlyAsnHisAspTyrTrpProGln 157
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Db        603 AGTCTCTTTCCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAG 662

Qy        158 AspGlnLeuSerValValThrSerLysValTyrAsnAlaValAlaAsnLeuTrpLysPro 177
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Db        663 GATCAACTGTCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCA 722

Qy        178 TrpLeuAspGluGluAlaIleSerThrLeuArgLysGlyGlyPheTyrSerGlnLysVal 197
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Db        723 TGGCTAGATGAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTT 782

Qy        198 ThrThrAsnProAsnLeuArgIleIleSerLeuAsnThrAsnLeuTyrTyrGlyProAsn 217
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Db        783 ACAACTAATCCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAAT 842

Qy        218 IleMetThrLeuAsnLysThrAspProAlaAsnGlnPheGluTrpLeuGluSerThrLeu 237
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Db        843 ATAATGACACTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTG 902

Qy        238 AsnAsnSerGlnGlnAsnLysGluLysValTyrIleIleAlaHisValProValGlyTyr 257
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Db        903 AACAACTCTCAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTAT 962

Qy        258 LeuProSerSerGlnAsnIleThrAlaMetArgGluTyrTyrAsnGluLysLeuIleAsp 277
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Db        963 CTGCCATCTTCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGAT 1022

Qy        278 IlePheGlnLysTyrSerAspValIleAlaGlyGlnPheTyrGlyHisThrHisArgAsp 297
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Db       1023 ATTTTTCAAAAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGAC 1082

Qy        298 SerIleMetValLeuSerAspLysLysGlySerProValAsnSerLeuPheValAlaPro 317
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Db       1083 AGCATTATGGTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCT 1142

Qy        318 AlaValThrProValLysSerValLeuGluLysGlnThrAsnAsnProGlyIleArgLeu 337
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Db       1143 GCTGTTACACCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTG 1202

Qy        338 PheGlnTyrAspProArgAspTyrLysLeuLeuAspMetLeuGlnTyrTyrLeuAsnLeu 357
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Db       1203 TTTCAGTATGATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTG 1262

Qy        358 ThrGluAlaAsnLeuLysGlyGluSerIleTrpLysLeuGluTyrIleLeuThrGlnThr 377
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Db       1263 ACAGAGGCGAATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACC 1322

Qy        378 TyrAspIleGluAspLeuGlnProGluSerLeuTyrGlyLeuAlaLysGlnPheThrIle 397
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Db       1323 TACGACATTGAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATC 1382

Qy        398 LeuAspSerLysGlnPheIleLysTyrTyrAsnTyrPhePheValSerTyrAspSerSer 417
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Db       1383 CTAGACAGTAAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGT 1442

Qy        418 ValThrCysAspLysThrCysLysAlaPheGlnIleCysAlaIleMetAsnLeuAspAsn 437
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Db       1443 GTAACATGTGATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAAT 1502

Qy        438 IleSerTyrAlaAspCysLeuLysGlnLeuTyrIleLysHisAsnTyr 453
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Db       1503 ATTTCCTATGCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTAC 1550

RESULT 11
AAI59324
ID   AAI59324 standard; cDNA; 1874 BP.
XX
AC   AAI59324;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 1527.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US034263.
XX
PR   23-DEC-1999;   99US-00471275.
PR   21-JAN-2000; 2000US-00488725.
PR   25-APR-2000; 2000US-00552317.
PR   20-JUN-2000; 2000US-00598042.
PR   19-JUL-2000; 2000US-00620312.
PR   03-AUG-2000; 2000US-00653450.
PR   14-SEP-2000; 2000US-00662191.
PR   19-OCT-2000; 2000US-00693036.
PR   29-NOV-2000; 2000US-00727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J,  Zhao QA;
PI   Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   P-PSDB; AAM40168.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders such
PT   as central nervous system injuries.
XX
PS   Claim 1; SEQ ID NO 1527; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC   encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
```

```
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders. Note: The sequence data for this patent did not form
CC   part of the printed specification
XX
SQ   Sequence 1874 BP; 596 A; 357 C; 334 G; 587 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.12e-204      Length:          1874
Score:                    2223.00        Matches:         416
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              91.59%         Indels:          0
DB:                       4              Gaps:            0

US-09-823-119B-1 (1-453) x AAI59324 (1-1874)

Qy         38 GlyGlnPheTrpHisValThrAspLeuHisLeuAspProThrTyrHisIleThrAspAsp 57
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Db        303 GGACAGTTTTGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGAC 362

Qy         58 HisThrLysValCysAlaSerSerLysGlyAlaAsnAlaSerAsnProGlyProPheGly 77
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Db        363 CACACAAAAGTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGA 422

Qy         78 AspValLeuCysAspSerProTyrGlnLeuIleLeuSerAlaPheAspPheIleLysAsn 97
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Db        423 GATGTTCTGTGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAAT 482

Qy         98 SerGlyGlnGluAlaSerPheMetIleTrpThrGlyAspSerProProHisValProVal 117
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Db        483 TCTGGACAAGAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTA 542

Qy        118 ProGluLeuSerThrAspThrValIleAsnValIleThrAsnMetThrThrThrIleGln 137
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Db        543 CCTGAACTCTCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAG 602

Qy        138 SerLeuProProAsnLeuGlnValProProAlaLeuGlyAsnHisAspTyrTrpProGln 157
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Db        603 AGTCTCTTTCCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAG 662

Qy        158 AspGlnLeuSerValValThrSerLysValTyrAsnAlaValAlaAsnLeuTrpLysPro 177
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Db        663 GATCAACTGTCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCA 722

Qy        178 TrpLeuAspGluGluAlaIleSerThrLeuArgLysGlyGlyPheTyrSerGlnLysVal 197
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Db        723 TGGCTAGATGAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTT 782

Qy        198 ThrThrAsnProAsnLeuArgIleIleSerLeuAsnThrAsnLeuTyrTyrGlyProAsn 217
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Db        783 ACAACTAATCCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAAT 842

Qy        218 IleMetThrLeuAsnLysThrAspProAlaAsnGlnPheGluTrpLeuGluSerThrLeu 237
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Db        843 ATAATGACACTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTG 902

Qy        238 AsnAsnSerGlnGlnAsnLysGluLysValTyrIleIleAlaHisValProValGlyTyr 257
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Db        903 AACAACTCTCAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTAT 962

Qy        258 LeuProSerSerGlnAsnIleThrAlaMetArgGluTyrTyrAsnGluLysLeuIleAsp 277
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Db        963 CTGCCATCTTCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGAT 1022

Qy        278 IlePheGlnLysTyrSerAspValIleAlaGlyGlnPheTyrGlyHisThrHisArgAsp 297
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Db       1023 ATTTTTCAAAAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGAC 1082

Qy        298 SerIleMetValLeuSerAspLysLysGlySerProValAsnSerLeuPheValAlaPro 317
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Db       1083 AGCATTATGGTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCT 1142

Qy        318 AlaValThrProValLysSerValLeuGluLysGlnThrAsnAsnProGlyIleArgLeu 337
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Db       1143 GCTGTTACACCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTG 1202

Qy        338 PheGlnTyrAspProArgAspTyrLysLeuLeuAspMetLeuGlnTyrTyrLeuAsnLeu 357
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Db       1203 TTTCAGTATGATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTG 1262

Qy        358 ThrGluAlaAsnLeuLysGlyGluSerIleTrpLysLeuGluTyrIleLeuThrGlnThr 377
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Db       1263 ACAGAGGCGAATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACC 1322

Qy        378 TyrAspIleGluAspLeuGlnProGluSerLeuTyrGlyLeuAlaLysGlnPheThrIle 397
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Db       1323 TACGACATTGAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATC 1382

Qy        398 LeuAspSerLysGlnPheIleLysTyrTyrAsnTyrPhePheValSerTyrAspSerSer 417
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Db       1383 CTAGACAGTAAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGT 1442

Qy        418 ValThrCysAspLysThrCysLysAlaPheGlnIleCysAlaIleMetAsnLeuAspAsn 437
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Db       1443 GTAACATGTGATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAAT 1502

Qy        438 IleSerTyrAlaAspCysLeuLysGlnLeuTyrIleLysHisAsnTyr 453
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Db       1503 ATTTCCTATGCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTAC 1550

RESULT 12
ADL62954
ID   ADL62954 standard; DNA; 2049 BP.
XX
AC   ADL62954;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human ovarian cancer DNA marker #21166.
XX
KW   Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
OS   Homo sapiens.
XX
PN   WO200170979-A2.
XX
PD   27-SEP-2001.
XX
PF   21-MAR-2001; 2001WO-US009126.
XX
PR   21-MAR-2000; 2000US-0191031P.
PR   25-MAY-2000; 2000US-0207124P.
PR   15-JUN-2000; 2000US-0211940P.
PR   07-JUL-2000; 2000US-0216820P.
PR   25-JUL-2000; 2000US-0220661P.
PR   21-DEC-2000; 2000US-0257672P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Lee J,  Lillie J;
XX
DR   WPI; 2001-611502/70.
XX
PT   Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT   cancer cells as compared to their normal non-cancerous ovarian cells are
PT   used to characterize stage, grade, histological type of ovarian cancer.
XX
PS   Disclosure; SEQ ID NO 21166; 106pp; English.
XX
CC   The invention relates to nucleic acid markers which are overexpressed in
CC   ovarian cancer cells as compared to their expression in normal (i.e. non-
CC   cancerous) ovarian cells. The invention also relates to polypeptides
CC   encoded by the markers, antibodies that selectively bind to the
CC   polypeptides, a method of inhibiting ovarian cancer in a patient at risk
```

CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.
XX
SQ Sequence 2049 BP; 614 A; 392 C; 415 G; 617 T; 0 U; 11 Other;

Alignment Scores:

Pred. No.:	3.51e-179	Length:	2049
Score:	1962.50	Matches:	380
Percent Similarity:	83.89%	Conservative:	0
Best Local Similarity:	83.89%	Mismatches:	2
Query Match:	80.86%	Indels:	72
DB:	5	Gaps:	1

US-09-823-119B-1 (1-453) x ADL62954 (1-2049)

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Qy          1 MetAlaLeuValArgAlaLeuValCysCysLeuLeuThrAlaTrpHisCysArgSerGly 20
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Db         99 ATGGCGCTGGTGCGCGCACTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCCGCTCCGGC 158

Qy         21 LeuGlyLeuProValAlaProAlaGlyGlyArgAsnProProProAlaIleGlyGlnPhe 40
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Db        159 CTCGGGCTGCCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGG------- 211

Qy         41 TrpHisValThrAspLeuHisLeuAspProThrTyrHisIleThrAspAspHisThrLys 60

Db        211 ------------------------------------------------------------ 211

Qy         61 ValCysAlaSerSerLysGlyAlaAsnAlaSerAsnProGlyProPheGlyAspValLeu 80

Db        211 ------------------------------------------------------------ 211

Qy         81 CysAspSerProTyrGlnLeuIleLeuSerAlaPheAspPheIleLysAsnSerGlyGln 100

Db        211 ------------------------------------------------------------ 211

Qy        101 GluAlaSerPheMetIleTrpThrGlyAspSerProProHisValProValProGluLeu 120
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Db        212 --------------------------GATAGCCCACCTCATGTTCCTGTACCTGAACTC 244

Qy        121 SerThrAspThrValIleAsnValIleThrAsnMetThrThrThrIleGlnSerLeuPhe 140
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Db        245 TCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTTT 304

Qy        141 ProAsnLeuGlnValPheProAlaLeuGlyAsnHisAspTyrTrpProGlnAspGlnLeu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 CCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAGGATCAACTG 364

Qy        161 SerValValThrSerLysValTyrAsnAlaValAlaAsnLeuTrpLysProTrpLeuAsp 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        365 CCTGTAGTCACCAGTAAAGTGTACAATGCAGTAGCAAACCTCTGGAAACCATGGCTAGAT 424

Qy        181 GluGluAlaIleSerThrLeuArgLysGlyGlyPheTyrSerGlnLysValThrThrAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 GAAGAAGCTATTAGTACTTTAAGGAAAGGTGGTTTTTATTCACAGAAAGTTACAACTAAT 484

Qy        201 ProAsnLeuArgIleIleSerLeuAsnThrAsnLeuTyrTyrGlyProAsnIleMetThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 CCAAACCTTAGGATCATCAGTCTAAACACAAACTTGTACTACGGCCCAAATATAATGACA 544

Qy        221 LeuAsnLysThrAspProAlaAsnGlnPheGluTrpLeuGluSerThrLeuAsnAsnSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 CTGAACAAGACTGACCCAGCCAACCAGTTTGAATGGCTAGAAAGTACATTGAACAACTCT 604

Qy        241 GlnGlnAsnLysGluLysValTyrIleIleAlaHisValProValGlyTyrLeuProSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 CAGCAGAATAAGGAGAAGGTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATCT 664

Qy        261 SerGlnAsnIleThrAlaMetArgGluTyrTyrAsnGluLysLeuIleAspIlePheGln 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        665 TCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCAA 724

Qy        281 LysTyrSerAspValIleAlaGlyGlnPheTyrGlyHisThrHisArgAspSerIleMet 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        725 AAATACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTATG 784

Qy        301 ValLeuSerAspLysLysGlySerProValAsnSerLeuPheValAlaProAlaValThr 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        785 GTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACA 844

Qy        321 ProValLysSerValLeuGluLysGlnThrAsnAsnProGlyIleArgLeuPheGlnTyr 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        845 CCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTAT 904

Qy        341 AspProArgAspTyrLysLeuLeuAspMetLeuGlnTyrTyrLeuAsnLeuThrGluAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        905 GATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGCG 964

Qy        361 AsnLeuLysGlyGluSerIleTrpLysLeuGluTyrIleLeuThrGlnThrTyrAspIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        965 AATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACATT 1024

Qy        381 GluAspLeuGlnProGluSerLeuTyrGlyLeuAlaLysGlnPheThrIleLeuAspSer 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1025 GAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAGT 1084

Qy        401 LysGlnPheIleLysTyrTyrAsnTyrPhePheValSerTyrAspSerSerValThrCys 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1085 AAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATGT 1144

Qy        421 AspLysThrCysLysAlaPheGlnIleCysAlaIleMetAsnLeuAspAsnIleSerTyr 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1145 GATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTAT 1204

Qy        441 AlaAspCysLeuLysGlnLeuTyrIleLysHisAsnTyr 453
              ||||||||||||||||||||||||||||||||||||||
Db       1205 GCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTAC 1243
```

RESULT 13
ABI99482
ID ABI99482 standard; cDNA; 1758 BP.
XX
AC ABI99482;
XX
DT 07-MAR-2002 (first entry)
XX
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:444.
XX
KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX
OS Mus musculus.
XX

PN WO200188188-A2.
XX
PD 22-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-JP004192.
XX
PR 18-MAY-2000; 2000JP-00145977.
XX
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX
PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX
DR WPI; 2002-034733/04.
DR P-PSDB; ABB57183.
XX
PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or by
PT determining the expression profile of a gene group comprising these
PT genes.
XX
PS Claim 2; Page 1248-1251; 2690pp; English.
XX
CC The present invention describes a method for examining ischaemic
CC conditions, comprising measuring the expression levels of particular
CC genes (I) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (I). The method
CC is useful for examining the ischaemic condition (e.g. compressive
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC expression levels of particular genes (ABI99202 to ABI99912, encoding the
CC protein sequences in ABB57020 to ABB57374) or by determining the
CC expression profile of a gene group comprising these genes. The expression
CC levels or expression profiles produced by these genes are used as an
CC indicator when screening for ischaemic condition-improving drugs or
CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
CC primers for a mouse ischaemic condition related sequence, which are used
CC in the exemplification of the present invention
XX
SQ Sequence 1758 BP; 493 A; 415 C; 386 G; 462 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.:	2.09e-178	Length:	1758
Score:	1953.50	Matches:	359
Percent Similarity:	88.96%	Conservative:	44
Best Local Similarity:	79.25%	Mismatches:	47
Query Match:	80.49%	Indels:	4
DB:	6	Gaps:	1

US-09-823-119B-1 (1-453) x ABI99482 (1-1758)

```
Qy          1 MetAlaLeuValArgAlaLeuValCysCysLeuLeuThrAlaTrpHisCysArgSerGly 20
              |||||||||:::         :::|||||||||||||   ||||||   |||      |||
Db         93 ATGGCGTTGCTGGGCAACTTCCTTTGCTGCCTACTGGTTGCCTGGCTCTGCGGCCCGGGG 152

Qy         21 LeuGlyLeuProValAlaProAlaGlyGlyArgAsnProProProAlaIleGlyGlnPhe 40
              ||||||:::|||:::|||||||||          :::      ||||||:::|||||||||
Db        153 CTCGGGGTGCCCCTGGCGCCGGCG---------GATCGCGCCCCAGCTGTGGGGCAGTTT 203

Qy         41 TrpHisValThrAspLeuHisLeuAspProThrTyrHisIleThrAspAspHisThrLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        204 TGGCACGTGACTGACTTACATCTAGACCCTACTTACCACATTACAGATGACCGTACCAAG 263

Qy         61 ValCysAlaSerSerLysGlyAlaAsnAlaSerAsnProGlyProPheGlyAspValLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GTGTGTGCTTCATCTAAAGGCGCAAATGCCTCCAACCCTGGGCCTTTCGGAGATGTCCTG 323

Qy         81 CysAspSerProTyrGlnLeuIleLeuSerAlaPheAspPheIleLysAsnSerGlyGln 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 TGTGACTCTCCATATCAACTTATTTTGTCAGCCTTTGATTTTATTAAGAATTCAGGACAA 383

Qy        101 GluAlaSerPheMetIleTrpThrGlyAspSerProProHisValProValProGluLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 GAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTGCCAGTACCTGAACTC 443

Qy        121 SerThrAspThrValIleAsnValIleThrAsnMetThrThrThrIleGlnSerLeuPhe 140
              ||||||   |||||||||   ||||||||||||||||||   |||:::|||:::||||||
Db        444 TCCACAGGCACCGTGATAAAGGTGATCACTAACATGACAATGACTGTCCAGAACCTGTTT 503

Qy        141 ProAsnLeuGlnValPheProAlaLeuGlyAsnHisAspTyrTrpProGlnAspGlnLeu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CCAAACCTCCAGGTTTTCCCTGCACTGGGCAATCATGACTACTGGCCACAGGACCAGCTG 563

Qy        161 SerValValThrSerLysValTyrAsnAlaValAlaAsnLeuTrpLysProTrpLeuAsp 180
                 :::|||||||||||||||||:::|||||||||:::|||||||||||||||||||||
Db        564 CCAATAGTCACCAGTAAGGTCTACAGTGCTGTGGCTGACCTCTGGAAACCCTGGCTGGGT 623

Qy        181 GluGluAlaIleSerThrLeuArgLysGlyGlyPheTyrSerGlnLysValThrThrAsn 200
              ||||||||||||||||||||:::|||||||||||||||||||||||||   :::|||
Db        624 GAAGAAGCTATTAGCACTTTAAAGAAAGGTGGTTTTTACTCACAGAAAGTTGCAAGTAAT 683

Qy        201 ProAsnLeuArgIleIleSerLeuAsnThrAsnLeuTyrTyrGlyProAsnIleMetThr 220
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 CCAGGCTTGAGGATCATTAGCCTAAACACAAACTTGTACTATGGCCCAAACATCATGACC 743

Qy        221 LeuAsnLysThrAspProAlaAsnGlnPheGluTrpLeuGluSerThrLeuAsnAsnSer 240
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||:::|||
Db        744 CTGAACAAGACAGACCCAGCAAATCAGTTTGAATGGCTGGAAAATACACTCAACAGCTCT 803

Qy        241 GlnGlnAsnLysGluLysValTyrIleIleAlaHisValProValGlyTyrLeuProSer 260
                    ||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        804 CTATGGAATAAGGAGAAGGTATACMTCATAGCGCATGTTCCAGTGGGCTATCTCCCTTAT 863

Qy        261 SerGlnAsnIleThrAlaMetArgGluTyrTyrAsnGluLysLeuIleAspIlePheGln 280
              :::   :::      |||:::|||:::|||||||||||||||:::|||||||||:::
Db        864 GCAACTGACACCCCGGCGATAAGGCAGTACTATAATGAGAAACTGCTTGATATTTTCAGA 923

Qy        281 LysTyrSerAspValIleAlaGlyGlnPheTyrGlyHisThrHisArgAspSerIleMet 300
              :::||||||   ||||||||||||||||||||||||||||||||||||||:::|||
Db        924 AGATACAGCTCCGTCATTGCGGGACAGTTCTATGGCCACACCCATAGAGACAGCCTTATG 983

Qy        301 ValLeuSerAspLysLysGlySerProValAsnSerLeuPheValAlaProAlaValThr 320
              ||||||||||||      |||:::|||:::||||||:::||||||||||||||||||||
Db        984 GTCCTTTCAGATAANAACGGGAATCCACTCAATTCTGTGTTTGTGGCACCTGCTGTTACA 1043

Qy        321 ProValLysSerValLeuGluLysGlnThrAsnAsnProGlyIleArgLeuPheGlnTyr 340
              |||||||||   ||||||:::|||:::|||||||||||||:::|||||||||||||||
Db       1044 CCAGTGAAAGGAGTTTTACAAAAGGAGACCAACAATCCCGGTGTCCGCCTATTTCAGTAC 1103

Qy        341 AspProArgAspTyrLysLeuLeuAspMetLeuGlnTyrTyrLeuAsnLeuThrGluAla 360
                 |||   ||||||   ||||||||||||:::|||||||||||||||||||||||||||
Db       1104 AAGCCTGGTGATTACACATTGCTGGACATGGTGCAGTATTACTTGAACTTGACAGAAGCC 1163

Qy        361 AsnLeuLysGlyGluSerIleTrpLysLeuGluTyrIleLeuThrGlnThrTyrAspIle 380
              ||||||||||||||||||   |||   ||||||||:::|||||||||   |||   :::
Db       1164 AATCTAAAAGGAGAATCCAACTGGACATTGGAGTATGTCTTGACTCAGGCCTACAGTGTT 1223

Qy        381 GluAspLeuGlnProGluSerLeuTyrGlyLeuAlaLysGlnPheThrIleLeuAspSer 400
              ||||||||||||:::|||||||||   |||   :::||||||          ||||||
Db       1224 GCAGATCTGCAGCCAAAGAGTTTATATGCCTTAGTTCAGCAATTTGCCACCAAAGACAGC 1283

Qy        401 LysGlnPheIleLysTyrTyrAsnTyrPhePheValSerTyrAspSerSerValThrCys 420
              |||||||||:::|||||||||:::|||:::||||||||||||||||||||   ||||||
Db       1284 AAGCAGTTCCTGAAATACTACCATTATTATTTTGTGAGTTATGACAGCAGTGCAACTTGT 1343

Qy        421 AspLysThrCysLysAlaPheGlnIleCysAlaIleMetAsnLeuAspAsnIleSerTyr 440
              |||:::   ||||||      |||:::|||||||||||||||||||:::::|||||||
Db       1344 GACCAGCATTGTAAGACCTTACAGGTCTGTGCAATTATGAATCTTGATAGCATGTCCTAT 1403

Qy        441 AlaAspCysLeuLysGlnLeuTyrIleLysHisAsnTyr 453
              ||||||||||||||   :::|||||||||::::::
Db       1404 GATGATTGCCTTAAACAGCA-TTTATAAAGCACAGTCAC 1441
```

RESULT 14
AAD21344
ID AAD21344 standard; cDNA; 1095 BP.
XX
AC AAD21344;

```
XX
DT   28-JAN-2002  (first entry)
XX
DE   Human nuclear factor kappaB-inducing factor (NFIF)-7a cDNA.
XX
KW   Human; NFkappaB; nuclear factor kappaB inducing factor; NFIF-14b;
KW   NFIF-7a; immune response; inflammatory response; atherosclerosis;
KW   rheumatoid arthritis; NSAID-induced gastropathy; scrapie; sepsis;
KW   neurodegenerative disease; autoimmune disease; antisense therapy;
KW   renal disease; restenosis; brain injury; viral disease; apoptosis;
KW   Alzheimer's disease; pleiotropic cytokine; gene therapy; asthma;
KW   Crohn's disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1095
FT                   /*tag=  a
FT                   /product= "Human NFIF-7a protein"
XX
PN   WO200174900-A2.
XX
PD   11-OCT-2001.
XX
PF   02-APR-2001; 2001WO-US010719.
XX
PR   31-MAR-2000; 2000US-0193905P.
PR   26-JUL-2000; 2000GB-00018307.
XX
PA   (AVET ) AVENTIS PHARM PROD INC.
XX
PI   Kaplow J,  Haws T,  Rosier M,  Denefle P;
XX
DR   WPI; 2001-662967/76.
DR   P-PSDB; AAE13019.
XX
PT   Novel isolated nuclear factor kappaB-inducing factor polypeptides (NFIF-
PT   7a, NFIF-14b), useful for increasing NFkappaB induction in patient, and
PT   for manufacturing medicaments for treating or preventing atherosclerosis.
XX
PS   Claim 2; Fig 3; 87pp; English.
XX
CC   The invention relates to nuclear factor kappaB (NFkappaB) inducing factor
CC   NFIF-14b, NFIF-7a (splice variant of NFIF14b) polypeptides and
CC   polynucleotides. NFIF-14b and NFIF-7a sequences are useful for inducing
CC   NFkappaB in vivo for increasing the activity of NFkappaB- regulated
CC   pathways including immune responses. Compositions comprising NFIF
CC   sequences are useful for treating or preventing NFkappaB-regulated
CC   inflammatory response such as rheumatoid arthritis, atherosclerosis,
CC   autoimmune diseases, viral diseases, NSAID-induced gastropathy,
CC   neurodegenerative diseases, scrapie, sepsis, apoptosis, Crohn's disease,
CC   renal disease, restenosis, brain injury/inflammation, Alzheimer's
CC   disease, asthma and improperly regulated expression of pleiotropic
CC   cytokines. They are also useful for inhibiting or lowering the expression
CC   of NFIF genes or polypeptides, respectively and thus for inhibiting
CC   induction of NFkappaB and consequently inhibiting or preventing NFkappaB-
CC   regulated immune responses that result in atherosclerosis and other
CC   diseases. Polynucleotides of the invention are useful in gene therapy and
CC   antisense therapy. The present sequence is human NFIF-7a cDNA
XX
SQ   Sequence 1095 BP; 317 A; 237 C; 224 G; 317 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                7.2e-174      Length:          1095
Score:                    1903.50       Matches:         364
Percent Similarity:       80.35%        Conservative:    0
Best Local Similarity:    80.35%        Mismatches:      0
Query Match:              78.43%        Indels:          89
DB:                       4             Gaps:            1

US-09-823-119B-1 (1-453) x AAD21344 (1-1095)

Qy          1 MetAlaLeuValArgAlaLeuValCysCysLeuLeuThrAlaTrpHisCysArgSerGly 20
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Db          1 ATGGCGCTGGTGCGCGCACTCGTCTGCTGCCTGCTGACTGCCTGGCACTGCCGCTCCGGC 60

Qy         21 LeuGlyLeuProValAlaProAlaGlyGlyArgAsnProProProAlaIleGlyGlnPhe 40

Db         61 CTCGGGCTGCCCGTGGCGCCCGCAGGCGGCAGGAATCCTCCTCCGGCGATAGGACAGTTT 120

Qy         41 TrpHisValThrAspLeuHisLeuAspProThrTyrHisIleThrAspAspHisThrLys 60

Db        121 TGGCATGTGACTGACTTACACTTAGACCCTACTTACCACATCACAGATGACCACACAAAA 180

Qy         61 ValCysAlaSerSerLysGlyAlaAsnAlaSerAsnProGlyProPheGlyAspValLeu 80

Db        181 GTGTGTGCTTCATCTAAAGGTGCAAATGCCTCCAACCCTGGCCCTTTTGGAGATGTTCTG 240

Qy         81 CysAspSerProTyrGlnLeuIleLeuSerAlaPheAspPheIleLysAsnSerGlyGln 100

Db        241 TGTGATTCTCCATATCAACTTATTTTGTCAGCATTTGATTTTATTAAAAATTCTGGACAA 300

Qy        101 GluAlaSerPheMetIleTrpThrGlyAspSerProProHisValProValProGluLeu 120

Db        301 GAAGCATCTTTCATGATATGGACAGGGGATAGCCCACCTCATGTTCCTGTACCTGAACTC 360

Qy        121 SerThrAspThrValIleAsnValIleThrAsnMetThrThrThrIleGlnSerLeuPhe 140

Db        361 TCAACAGACACTGTTATAAATGTGATCACTAATATGACAACCACCATCCAGAGTCTCTTT 420

Qy        141 ProAsnLeuGlnValPheProAlaLeuGlyAsnHisAspTyrTrpProGlnAspGlnLeu 160

Db        421 CCAAATCTCCAGGTTTTCCCTGCGCTGGGTAATCATGACTATTGGCCACAG--------- 471

Qy        161 SerValValThrSerLysValTyrAsnAlaValAlaAsnLeuTrpLysProTrpLeuAsp 180

Db        471 ------------------------------------------------------------ 471

Qy        181 GluGluAlaIleSerThrLeuArgLysGlyGlyPheTyrSerGlnLysValThrThrAsn 200

Db        471 ------------------------------------------------------------ 471

Qy        201 ProAsnLeuArgIleIleSerLeuAsnThrAsnLeuTyrTyrGlyProAsnIleMetThr 220

Db        471 ------------------------------------------------------------ 471

Qy        221 LeuAsnLysThrAspProAlaAsnGlnPheGluTrpLeuGluSerThrLeuAsnAsnSer 240

Db        471 ------------------------------------------------------------ 471

Qy        241 GlnGlnAsnLysGluLysValTyrIleIleAlaHisValProValGlyTyrLeuProSer 260

Db        472 ------------------GTGTATATCATAGCACATGTTCCAGTGGGGTATCTGCCATCT 513

Qy        261 SerGlnAsnIleThrAlaMetArgGluTyrTyrAsnGluLysLeuIleAspIlePheGln 280

Db        514 TCACAGAACATCACAGCAATGAGAGAATACTATAATGAGAAATTGATAGATATTTTTCAA 573

Qy        281 LysTyrSerAspValIleAlaGlyGlnPheTyrGlyHisThrHisArgAspSerIleMet 300

Db        574 AAGTACAGTGATGTCATTGCAGGACAATTTTATGGACACACTCACAGAGACAGCATTATG 633

Qy        301 ValLeuSerAspLysLysGlySerProValAsnSerLeuPheValAlaProAlaValThr 320

Db        634 GTTCTTTCAGATAAAAAAGGAAGTCCAGTAAATTCTTTGTTTGTGGCTCCTGCTGTTACA 693

Qy        321 ProValLysSerValLeuGluLysGlnThrAsnAsnProGlyIleArgLeuPheGlnTyr 340

Db        694 CCAGTGAAGAGTGTTTTAGAAAAACAGACCAACAATCCTGGTATCAGACTGTTTCAGTAT 753

Qy        341 AspProArgAspTyrLysLeuLeuAspMetLeuGlnTyrTyrLeuAsnLeuThrGluAla 360

Db        754 GATCCTCGTGATTATAAATTATTGGATATGTTGCAGTATTACTTGAATCTGACAGAGGCG 813

Qy        361 AsnLeuLysGlyGluSerIleTrpLysLeuGluTyrIleLeuThrGlnThrTyrAspIle 380
```

```
Db        814 AATCTAAAGGGAGAGTCCATCTGGAAGCTGGAGTATATCCTGACCCAGACCTACGACATT 873

Qy        381 GluAspLeuGlnProGluSerLeuTyrGlyLeuAlaLysGlnPheThrIleLeuAspSer 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 GAAGATTTGCAGCCGGAAAGTTTATATGGATTAGCTAAACAATTTACAATCCTAGACAGT 933

Qy        401 LysGlnPheIleLysTyrTyrAsnTyrPhePheValSerTyrAspSerSerValThrCys 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 AAGCAGTTTATAAAATACTACAATTACTTCTTTGTGAGTTATGACAGCAGTGTAACATGT 993

Qy        421 AspLysThrCysLysAlaPheGlnIleCysAlaIleMetAsnLeuAspAsnIleSerTyr 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 GATAAGACATGTAAGGCCTTTCAGATTTGTGCAATTATGAATCTTGATAATATTTCCTAT 1053

Qy        441 AlaAspCysLeuLysGlnLeuTyrIleLysHisAsnTyr 453
              |||||||||||||||||||||||||||||||||||||||
Db       1054 GCAGATTGCCTCAAACAGCTTTATATAAAGCACAATTAC 1092

RESULT 15
AAA02374
ID   AAA02374 standard; cDNA; 728 BP.
XX
AC   AAA02374;
XX
DT   19-MAY-2000  (first entry)
XX
DE   Human colon cancer cell line polynucleotide sequence SEQ ID NO:2365.
XX
KW   Human; colon cancer; tumour; diagnosis; gene expression product; probe;
KW   detection; cancerous state; metastasis; identification; breast cancer;
KW   oestrogen receptor-positive breast cancer; therapy;
KW   oestrogen receptor-negative breast cancer; lung cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9958675-A2.
XX
PD   18-NOV-1999.
XX
PF   13-MAY-1999;   99WO-US010602.
XX
PR   14-MAY-1998;   98US-0085426P.
PR   15-MAY-1998;   98US-0085537P.
PR   15-MAY-1998;   98US-0085696P.
PR   21-OCT-1998;   98US-0105234P.
PR   27-OCT-1998;   98US-0105877P.
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Williams LT,  Escobedo J,  Innis MA,  Garcia PD,  Sudduth-Klinger J;
PI   Reinhard C,  Giese K,  Randazzo F,  Kennedy GC,  Pot D,  Kassam A;
PI   Lamson G,  Drmanac R,  Crkvenjakov R,  Dickson M,  Drmanac S,  Labat I;
PI   Leshkowitz D,  Kita D,  Garcia V,  Jones LW,  Stache-Crain B;
XX
DR   WPI; 2000-126369/11.
XX
PT   Polynucleotide library used to determine cancerous states of mammalian
PT   cells.
XX
PS   Claim 1; Page 940; 1097pp; English.
XX
CC   AAA00010 to AAA02716 represent polynucleotides isolated from cDNA
CC   libraries constructed from human colon cancer cell lines. The present
CC   invention also describes a method of detecting differentially expressed
CC   genes correlated with a cancerous state of a mammalian cell, comprising
CC   detecting at least one differentially expressed gene product in a test
CC   sample derived from a cell suspected of being cancerous, where detection
CC   of the differentially expressed gene product is correlated with a
CC   cancerous state of the cell from which the test sample was derived. The
CC   polynucleotides sequences can be used in a method for detecting
CC   differentially expressed genes correlated with a cancerous state of a
CC   mammalian cell. The polynucleotides can also be used as probes for
CC   detecting and mapping related genes. They can be used in diagnosis and
CC   prognosis of diseases and disorders (e.g. identification of pre-
CC   metastatic or metastatic cancerous states, stages of cancer, or
CC   responsiveness of cancer to therapy). This is particularly for breast
CC   cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
CC   negative breast cancer, lung cancer, and colon cancer
XX
SQ   Sequence 728 BP; 240 A; 155 C; 139 G; 189 T; 0 U; 5 Other;

Alignment Scores:
Pred. No.:                4.9e-107      Length:          728
Score:                    1209.00       Matches:         230
Percent Similarity:       98.71%        Conservative:    0
Best Local Similarity:    98.71%        Mismatches:      3
Query Match:              49.81%        Indels:          0
DB:                       3             Gaps:            0

US-09-823-119B-1 (1-453) x AAA02374 (1-728)

Qy        110 AspSerProProHisValProValProGluLeuSerThrAspThrValIleAsnValIle 129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         28 GATAGCCCACCTCATGTTCCTGTACCTGAACTCTCAACAGACACTGTTATAAATGTGATC 87

Qy        130 ThrAsnMetThrThrThrIleGlnSerLeuProAsnLeuGlnValProAlaLeu 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 ACTAATATGACAACCACCATCCAGAGTCTCTTTCCAAATCTCCAGGTTTTCCCTGCGCTG 147

Qy        150 GlyAsnHisAspTyrTrpProGlnAspGlnLeuSerValValThrSerLysValTyrAsn 169
              |||||||||||||||||||||||||||||||    |||||||||||||||||||||||||
Db        148 GGTAATCATGACTATTGGCCACAGGATCAACTGCCTGTAGTCACCAGTAAAGTGTACAAT 207

Qy        170 AlaValAlaAsnLeuTrpLysProTrpLeuAspGluGluAlaIleSerThrLeuArgLys 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 GCAGTAGCAAACCTCTGGAAACCATGGCTAGATGAAGAAGCTATTAGTACTTTAAGGAAA 267

Qy        190 GlyGlyPheTyrSerGlnLysValThrThrAsnProAsnLeuArgIleIleSerLeuAsn 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 GGTGGTTTTTATTCACAGAAAGTTACAACTAATCCAAACCTTAGGATCATCAGTCTAAAC 327

Qy        210 ThrAsnLeuTyrTyrGlyProAsnIleMetThrLeuAsnLysThrAspProAlaAsnGln 229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 ACAAACTTGTACTACGGCCCAAATATAATGACACTGAACAAGACTGACCCAGCCAACCAG 387

Qy        230 PheGluTrpLeuGluSerThrLeuAsnAsnSerGlnGlnAsnLysGluLysValTyrIle 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 TTTGAATGGCTAGAAAGTACATTGAACAACTCTCAGCAGAATAAGGAGAAGGTGTATATC 447

Qy        250 IleAlaHisValProValGlyTyrLeuProSerSerGlnAsnIleThrAlaMetArgGlu 269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 ATAGCACATGTTCCAGTGGGGTATCTGCCATCTTCACAGAACATCACAGCAATGAGAGAA 507

Qy        270 TyrTyrAsnGluLysLeuIleAspIlePheGlnLysTyrSerAspValIleAlaGlyGln 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 TACTATAATGAGAAATTGATAGATATTTTTCAAAAATACAGTGATGTCATTGCAGGACAA 567

Qy        290 PheTyrGlyHisThrHisArgAspSerIleMetValLeuSerAspLysLysGlySerPro 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 TTTTATGGACACACTCACAGAGACAGCATTATGGTTCTTTCAGATAAAAAAGGAAGTCCA 627

Qy        310 ValAsnSerLeuPheValAlaProAlaValThrProValLysSerValLeuGluLysGln 329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        628 GTAAATTCTTTGTTTGTGGCTCCTGCTGTTACACCAGTGAAGAGTGTTTTAGAAAAACAG 687

Qy        330 ThrAsnAsnProGlyIleArgLeuPheGlnTyrAspPro 342
              |||||||||   ||||||||||||   ||||||||||||
Db        688 ACCAACAATNCTGGTATCAGACTGGTTCAGTATGATCCT 726


Search completed: April  5, 2005, 13:24:41
Job time : 654 secs
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